

SEQUENCE LISTING

(1) GENERAL INFORMATION:

Sub B1

(i) APPLICANT: Hilton, Douglas J.
Alexander, Warren S.
Viney, Elizabeth M.
Willson, Tracy A.
Richardson, Rachael T.
Starr, Robyn
Nicholson, Sandra E.
Metcalf, Donald
Nicola, Nicos A.

(ii) TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS

(iii) NUMBER OF SEQUENCES: 50

(iv) CORRESPONDENCE ADDRESS:

G1

(A) ADDRESSEE: Scully, Scott, Murphy & Presser
(B) STREET: 400 Garden City Plaza
(C) CITY: Garden City, New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 11530

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

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(vi) PRIOR APPLICATION DATA:

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(B) FILING DATE: 01-NOV-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: DiGiglio, Frank S.
(B) REGISTRATION NO: 31,346
(C) REFERENCE/DOCKET NUMBER: 10976

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (516) 742-4343
- (B) TELEFAX: (516) 742-4366
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACGCCGCCC ACGTGAAGGC

20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTCGCCAATG ACAAGACGCT

20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGAGGCTCAA GCTCCGGGCG GATTCTGCGT GCCGCTCTCG CTCCTTGGGG TCTGTTGGCC

-101

GGCCTGTGCC	ACCCGGACGC	CCGGCTCACT	GCCTCTGTCT	CCCCCATCAG	CGCAGCCCCG	-41
GACGCTATGG	CCCACCCCTC	CAGCTGGCCC	CTCGAGTAGG			-1
ATG GTA GCA CGC AAC CAG GTG GCA GCC GAC AAT GCG ATC TCC CCG GCA	Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala	48				
1 5 10 15						
GCA GAG CCC CGA CGG CGG TCA GAG CCC TCC TCG TCC TCG TCT TCG TCC	Ala Glu Pro Arg Arg Arg Ser Glu Pro Ser Ser Ser Ser Ser Ser Ser	96				
20 25 30						
TCG CCA GCG GCC CCC GTG CGT CCC CGG CCC TGC CCG GCG GTC CCA GCC	Ser Pro Ala Ala Pro Val Arg Pro Arg Pro Cys Pro Ala Val Pro Ala	144				
35 40 45						
CCA GCC CCT GGC GAC ACT CAC TTC CGC ACC TTC CGC TCC CAC TCC GAT	Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ser Asp	192				
50 55 60						
TAC CGG CGC ATC ACG CGG ACC AGC GCG CTC CTG GAC GCC TGC GGC TTC	Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe	240				
65 70 75 80						
TAT TGG GGA CCC CTG AGC GTG CAC GGG GCG CAC GAG CGG CTG CGT GCC	Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala	288				
85 90 95						
GAG CCC GTG GGC ACC TTC TTG GTG CGC GAC AGT CGT CAA CGG AAC TGC	Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys	336				
100 105 110						
TTC TTC GCG CTC AGC GTG AAG ATG GCT TCG GGC CCC ACG AGC ATC CGC	Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg	384				
115 120 125						
GTG CAC TTC CAG GCC GGC CGC TTC CAC TTG GAC GGC AGC CGC GAG ACC	Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr	432				
130 135 140						
TTC GAC TGC CTT TTC GAG CTG CTG GAG CAC TAC GTG GCG GCG CCG CGC	Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg	480				
145 150 155 160						
CGC ATG TTG GGG GCC CCG CTG CGC CAG CGC CGC GTG CGG CCG CTG CAG	Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln	528				
165 170 175						
GAG CTG TGT CGC CAG CGC ATC GTG GCC GCC GTG GGT CGC GAG AAC CTG	Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu	576				
180 185 190						

GCG CGC ATC CCT CTT AAC CCG GTA CTC CGT GAC TAC CTG AGT TCC TTC	624
Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe	
195 200 205	
CCC TTC CAG ATC TGA CCGGCTG CCGCTGTGCC GCAGCATTAA GTGGGGGCGC	676
Pro Phe Gln Ile *	
210	
CTTATTATTT CTTATTATTA ATTATTATTA TTTTCTGGA ACCACGTGGG AGCCCTCCCC	736
GCCTGGGTCG GAGGGAGTGG TTGTGGAGGG TGAGATGCCT CCCACTTCTG GCTGGAGACC	796
TCATCCCACC TCTCAGGGGT GGGGGTGCTC CCCTCCTGGT GCTCCCTCCG GGTCCCCCCT	856
GGTTGTAGCA GCTTGTGTCT GGGGCCAGGA CCTGAATTCC ACTCCTACCT CTCCATGTTT	916
ACATATTCCC AGTATCTTTG CACAAACCAG GGGTCGGGGA GGGTCTCTGG CTTCATTTTT	976
CTGCTGTGCA GAATATCCTA TTTTATATTT TTACAGCCAG TTAGGTAAT AAACCTTTATT	1036
ATGAAAGTTT TTTTTTAAAA GAAAAA AAAA	1075

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala	
1 5 10 15	
Ala Glu Pro Arg Arg Arg Ser Glu Pro Ser Ser Ser Ser Ser Ser Ser	
20 25 30	
Ser Pro Ala Ala Pro Val Arg Pro Arg Pro Cys Pro Ala Val Pro Ala	
35 40 45	
Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ser Asp	
50 55 60	
Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe	
65 70 75 80	
Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala	
85 90 95	

- 111 -

Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys
100 105 110
Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg
115 120 125
Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr
130 135 140
Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg
145 150 155 160
Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln
165 170 175
Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu
180 185 190
Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe
195 200 205
Pro Phe Gln Ile
210

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 223..819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGATCTGTG GGTGACAGTG TCTGCGAGAG ACTTTGCCAC ACCATTCTGC CGGAATTTGG 60
AGAAAAAGAA CCAGCCGCTT CCAGTCCCCT CCCCCTCCGC CACCATTTCG GACACCCTGC 120
ACACTCTCGT TTTGGGGTAC CCTGTGACTT CCAGGCAGCA CGCGAGGTCC ACTGGCCCCA 180
GCTCGGGCGA CCAGCTGTCT GGGACGTGTT GACTCATCTC CC ATG ACC CTG CGG 234
Met Thr Leu Arg
1

[illegible]

AAGATGTAGC TAGGTATTTT AAAGTTCCCC TTAGGTAGTT TTAGCTGAAT GATGCTTTCT	1046
TTCCTATGGC TGCTCAAGAT CAAATGGCCC TTTTAAATGA AACAAAACAA AACAAAACAA	1106
AAAAAAAAAA AAAAA	1121

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 198 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Thr	Leu	Arg	Cys	Leu	Glu	Pro	Ser	Gly	Asn	Gly	Ala	Asp	Arg	Thr
1				5					10					15	
Arg	Ser	Gln	Trp	Gly	Thr	Ala	Gly	Leu	Pro	Glu	Glu	Gln	Ser	Pro	Glu
		20						25					30		
Ala	Ala	Arg	Leu	Ala	Lys	Ala	Leu	Arg	Glu	Leu	Ser	Gln	Thr	Gly	Trp
		35					40					45			
Tyr	Trp	Gly	Ser	Met	Thr	Val	Asn	Glu	Ala	Lys	Glu	Lys	Leu	Lys	Glu
	50					55					60				
Ala	Pro	Glu	Gly	Thr	Phe	Leu	Ile	Arg	Asp	Ser	Ser	His	Ser	Asp	Tyr
65					70				75						80
Leu	Leu	Thr	Ile	Ser	Val	Lys	Thr	Ser	Ala	Gly	Pro	Thr	Asn	Leu	Arg
				85					90					95	
Ile	Glu	Tyr	Gln	Asp	Gly	Lys	Phe	Arg	Leu	Asp	Ser	Ile	Ile	Cys	Val
		100						105					110		
Lys	Ser	Lys	Leu	Lys	Gln	Phe	Asp	Ser	Val	Val	His	Leu	Ile	Asp	Tyr
		115					120					125			
Tyr	Val	Gln	Met	Cys	Lys	Asp	Lys	Arg	Thr	Gly	Pro	Glu	Ala	Pro	Arg
	130					135					140				
Asn	Gly	Thr	Val	His	Leu	Tyr	Leu	Thr	Lys	Pro	Leu	Tyr	Thr	Ser	Ala
145					150					155					160
Pro	Thr	Leu	Gln	His	Phe	Cys	Arg	Leu	Ala	Ile	Asn	Lys	Cys	Thr	Gly
				165					170					175	
Thr	Ile	Trp	Gly	Leu	Pro	Leu	Pro	Thr	Arg	Leu	Lys	Asp	Tyr	Leu	Glu
			180					185					190		

Glu Tyr Lys Phe Gln Val
195

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 18..695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGCTGGCTCC GTGCGCC ATG GTC ACC CAC AGC AAG TTT CCC GCC GCC GGG	50
Met Val Thr His Ser Lys Phe Pro Ala Ala Gly	
1 5 10	
ATG AGC CGC CCC CTG GAC ACC AGC CTG CGC CTC AAG ACC TTC AGC TCC	98
Met Ser Arg Pro Leu Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser	
15 20 25	
AAA AGC GAG TAC CAG CTG GTG GTG AAC GCC GTG CGC AAG CTG CAG GAG	146
Lys Ser Glu Tyr Gln Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu	
30 35 40	
AGC GGA TTC TAC TGG AGC GCC GTG ACC GGC GGC GAG GCG AAC CTG CTG	194
Ser Gly Phe Tyr Trp Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu	
45 50 55	
CTC AGC GCC GAG CCC GCG GGC ACC TTT CTT ATC CGC GAC AGC TCG GAC	242
Leu Ser Ala Glu Pro Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp	
60 65 70 75	
CAG CGC CAC TTC TTC ACG TTG AGC GTC AAG ACC CAG TCG GGG ACC AAG	290
Gln Arg His Phe Phe Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys	
80 85 90	
AAC CTA CGC ATC CAG TGT GAG GGG GGC AGC TTT TCG CTG CAG AGT GAC	338
Asn Leu Arg Ile Gln Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp	
95 100 105	
CCC CGA AGC ACG CAG CCA GTT CCC CGC TTC GAC TGT GTA CTC AAG CTG	386
Pro Arg Ser Thr Gln Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu	
110 115 120	

GTG CAC CAC TAC ATG CCG CCT CCA GGG ACC CCC TCC TTT TCT TTG CCA	434
Val His His Tyr Met Pro Pro Pro Gly Thr Pro Ser Phe Ser Leu Pro	
125 130 135	
CCC ACG GAA CCC TCG TCC GAA GTT CCG GAG CAG CCA CCT GCC CAG GCA	482
Pro Thr Glu Pro Ser Ser Glu Val Pro Glu Gln Pro Pro Ala Gln Ala	
140 145 150 155	
CTC CCC GGG AGT ACC CCC AAG AGA GCT TAC TAC ATC TAT TCT GGG GGC	530
Leu Pro Gly Ser Thr Pro Lys Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly	
160 165 170	
GAG AAG ATT CCG CTG GTA CTG AGC CGA CCT CTC TCC TCC AAC GTG GCC	578
Glu Lys Ile Pro Leu Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala	
175 180 185	
ACC CTC CAG CAT CTT TGT CGG AAG ACT GTC AAC GGC CAC CTG GAC TCC	626
Thr Leu Gln His Leu Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser	
190 195 200	
TAT GAG AAA GTG ACC CAG CTG CCT GGA CCC ATT CGG GAG TTC CTG GAT	674
Tyr Glu Lys Val Thr Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp	
205 210 215	
CAG TAT GAT GCT CCA CTT TAAGGAGCAA AAGGGTCAGA GGGGGCCTG	722
Gln Tyr Asp Ala Pro Leu	
220 225	
GGTCGGTCGG TCGCCTCTCC TCCGAGGCAC ATGGCACAAG CACAAAAATC CAGCCCCAAC	782
GGTCGGTAGC TCCCAGTGAG CCAGGGGCAG ATTGGCTTCT TCCTCAGGCC CTCCACTCCC	842
GCAGAGTAGA GCTGGCAGGA CCTGGAATTC GTCTGAGGGG AGGGGGAGCT GCCACCTGCT	902
TTCCCCCCTC CCCCAGCTCC AGCTTCTTTC AAGTGGAGCC AGCCGGCCTG GCCTGGTGGG	962
ACAATACCTT TGACAAGCGG ACTCTCCCCT CCCCTTCCTC CACACCCCCT CTGCTTCCCA	1022
AGGGAGGTGG GGACACCTCC AAGTGTGAA CTTAGAACTG CAAGGGGAAT CTTCAAACCTT	1082
TCCCGCTGGA ACTTGTTTGC GCTTTGATTT GGTTCGATCA AGAGCAGGCA CCTGGGGGAA	1142
GGATGGAAGA GAAAAGGGTG TGTGAAGGGT TTTTATGCTG GCCAAAGAAA TAACCACTCC	1202
CACTGCCCAA CCTAGGTGAG GAGTGGTGGC TCCTGGCTCT GGGGAGAGTG GCAAGGGGTG	1262
ACCTGAAGAG AGCTATACTG GTGCCAGGCT CCTCTCCATG GGGCAGCTAA TGAAACCTCG	1322
CAGATCCCTT GCACCCCAGA ACCCTCCCCG TTGTGAAGAG GCAGTAGCAT TTAGAAGGGA	1382
GACAGATGAG GCTGGTGAGC TGGCCGCCTT TTCCAACACC GAAGGGAGGC AGATCAACAG	1442
ATGAGCCATC TTGGAGCCCA GGTTCCTCCCT GGAGCAGATG GAGGGTTCTG CTTTGTCTCT	1502
CCTATGTGGG GCTAGGAGAC TCGCCTTAAA TGCCCTCTGT CCCAGGGATG GGGATTGGCA	1562

CACAAGGAGC CAAACACAGC CAATAGGCAG AGAGTTGAGG GATTCACCCA GGTGGCTACA	1622
GGCCAGGGGA AGTGGCTGCA GGGGAGAGAC CCAGTCACTC CAGGAGACTC CTGAGTTAAC	1682
ACTGGGAAGA CATTGGCCAG TCCTAGTCAT CTCTCGGTCA GTAGGTCCGA GAGCTTCCAG	1742
GCCCTGCACA GCCCTCCTTT CTCACCTGGG GGGAGGCAGG AGGTGATGGA GAAGCCTTCC	1802
CATGCCGCTC ACAGGGGCCT CACGGGAATG CAGCAGCCAT GCAATTACCT GGAACTGGTC	1862
CTGTGTTGGG GAGAAACAAG TTTTCTGAAG TCAGGTATGG GGCTGGGTGG GGCAGCTGTG	1922
TGTTGGGGTG GCTTTTTTCT CTCTGTTTTG AATAATGTTT ACAATTTGCC TCAATCACTT	1982
TTATAAAAAT CCACCTCCAG CCCGCCCTC TCCCCACTCA GGCCTTCGAG GCTGTCTGAA	2042
GATGCTTGAA AAACTCAACC AAATCCCAGT TCAACTCAGA CTTTGCACAT ATATTTATAT	2102
TTATACTCAG AAAAGAAACA TTTCAGTAAT TTATAATAAA AGAGCACTAT TTTTAAATGA	2162
AAAAAAAAAA AAAAAAAAAA AAAAA	2187

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Val	Thr	His	Ser	Lys	Phe	Pro	Ala	Ala	Gly	Met	Ser	Arg	Pro	Leu
1				5					10					15	
Asp	Thr	Ser	Leu	Arg	Leu	Lys	Thr	Phe	Ser	Ser	Lys	Ser	Glu	Tyr	Gln
			20					25					30		
Leu	Val	Val	Asn	Ala	Val	Arg	Lys	Leu	Gln	Glu	Ser	Gly	Phe	Tyr	Trp
		35					40					45			
Ser	Ala	Val	Thr	Gly	Gly	Glu	Ala	Asn	Leu	Leu	Leu	Ser	Ala	Glu	Pro
	50					55					60				
Ala	Gly	Thr	Phe	Leu	Ile	Arg	Asp	Ser	Ser	Asp	Gln	Arg	His	Phe	Phe
65					70					75					80
Thr	Leu	Ser	Val	Lys	Thr	Gln	Ser	Gly	Thr	Lys	Asn	Leu	Arg	Ile	Gln
				85					90					95	
Cys	Glu	Gly	Gly	Ser	Phe	Ser	Leu	Gln	Ser	Asp	Pro	Arg	Ser	Thr	Gln
			100					105					110		

Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met
 115 120 125
 Pro Pro Pro Gly Thr Pro Ser Phe Ser Leu Pro Pro Thr Glu Pro Ser
 130 135 140
 Ser Glu Val Pro Glu Gln Pro Pro Ala Gln Ala Leu Pro Gly Ser Thr
 145 150 155 160
 Pro Lys Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu
 165 170 175
 Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu
 180 185 190
 Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr
 195 200 205
 Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro
 210 215 220
 Leu
 225

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1094 base pairs .
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCCGGCTGG	CCCCTTCTGT	AGGATGGTAG	CACACAACCA	GGTGGCAGCC	GACAATGCAG	60
TCTCCACAGC	AGCAGAGCCC	CGACCGCGGC	CAGAACCTTC	CTCCTCTTCC	TCCTCCTCGC	120
CCGCGGCCCC	CGCGCGCCCC	CGGCCGTGCC	CCGCGGTCCC	GGCCCCGGCC	CCCGGCGACA	180
CGCACTTCCG	CACATTCCGT	TCGCACGCCG	ATTACCGGCG	CATCACGCGC	GCCAGCGCGC	240
TCCTGGACGC	CTGCGGATTC	TACTGGGGGC	CCCTGAGCGT	GCACGGGGCG	CACGAGCGGC	300
TGCGCGCCGA	GCCCGTGGGC	ACCTTCCTGG	TGCGCGACAG	CCGCCAGCGG	AACTGCTTTT	360
TCGCCCTTAG	CGTGAAGATG	GCCTCGGGAC	CCACGAGCAT	CCGCGTGAC	TTTCAGGCCG	420
GCCGCTTTCA	CCTGGATGGC	AGCCGCGAGA	GCTTCGACTG	CCTCTTCGAG	CTGCTGGAGC	480
ACTACGTGGC	GGCGCCGCGC	CGCATGCTGG	GGGCCCCGCT	GCGCCAGCGC	CGCGTGCGGC	540

CGCTGCAGGA	GCTGTGCCGC	CAGCGCATCG	TGGCCACCGT	GGGCCGCGAG	AACCTGGCTC	600
GCATCCCCCT	CAACCCCGTC	CTCCGCGACT	ACCTGAGCTC	CTTCCCCTTC	CAGATTTGAC	660
CGGCAGCGCC	CGCCGTGCAC	GCAGCATTAA	CTGGGATGCC	GTGTTATTTT	GTTATTACTT	720
GCCTGGAACC	ATGTGGGTAC	CCTCCCCGGC	CTGGGTTGGA	GGGAGCGGAT	GGGTGTAGGG	780
GCGAGGCGCC	TCCCGCCCTC	GGCTGGGAGAC	GAGGCCGCAG	ACCCCTTCTC	ACCTCTTGAG	840
GGGGTCCTCC	CCCTCCTGGT	GCTCCCTCTG	GGTCCCCCTG	GTTGTTGTAG	CAGCTTAACT	900
GTATCTGGAG	CCAGGACCTG	AACTCGCACC	TCCTACCTCT	TCATGTTTAC	ATATACCCAG	960
TATCTTTGCA	CAAACCAGGG	GTTGGGGGAG	GGTCTCTGGC	TTTATTTTTC	TGCTGTGCAG	1020
AATCCTATTT	TATATTTTTT	AAAGTCAGTT	TAGGTAATAA	ACTTTATTAT	GAAAGTTTTT	1080
TTTTTTAAAA	AAAA					1094

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Val	Ala	His	Asn	Gln	Val	Ala	Ala	Asp	Asn	Ala	Val	Ser	Thr	Ala	1	5	10	15
Ala	Glu	Pro	Arg	Arg	Arg	Pro	Glu	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Ser	20	25	30	
Pro	Ala	Ala	Pro	Ala	Arg	Pro	Arg	Pro	Cys	Pro	Ala	Val	Pro	Ala	Pro	35	40	45	
Ala	Pro	Gly	Asp	Thr	His	Phe	Arg	Thr	Phe	Arg	Ser	His	Ala	Asp	Tyr	50	55	60	
Arg	Arg	Ile	Thr	Arg	Ala	Ser	Ala	Leu	Leu	Asp	Ala	Cys	Gly	Phe	Tyr	65	70	75	80
Trp	Gly	Pro	Leu	Ser	Val	His	Gly	Ala	His	Glu	Arg	Leu	Arg	Ala	Glu	85	90	95	

Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys Phe
 100 105 110
 Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg Val
 115 120 125
 His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Ser Phe
 130 135 140
 Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg Arg
 145 150 155 160
 Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln Glu
 165 170 175
 Leu Cys Arg Gln Arg Ile Val Ala Thr Val Gly Arg Glu Asn Leu Ala
 180 185 190
 Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe Pro
 195 200 205
 Phe Gln Ile
 210

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2807 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAAACCGAG GCGGGGAGAC CAGCAGGCCT TGGCCTCAGA GCTTCAGAGT CGCGTGGCAG 60
 CAAACAGAGA AACCTGTAGA GGGCAGTGTG CGTCACTTAG CTCAGGGAAG CTGCACGCGA 120
 AACTCACCCG CCTTCATTCA TAAACATCGT CAGCTAGGCA CCTACTCCTG GGCTTTCAGG 180
 ACAAACTGAA TCACGAAACC ACAGTGTCTT TAAAATAGGT CTGACCGCCT GAATCCCTGG 240
 CCAAGGTGTG TACGGGGCAT GGGAGCCCTT GTGCAGAGAT GCTTGCAGGA GCCTTGAGGG 300
 GCTCTGTAAG ACAGAGGCTA GGAAGACAAA GTTGGGGGCT ACAGCTTCTT GTCCTGCCCCG 360
 GGGCCTCAGT TTCTTCGGTT GCCCACGTAG GAGTGCAGAG AGTCCAGCCC CTGGGGACCC 420
 AACCCAACCC CGCCAGTTT CCGAGGAACT CGTCCGGGAG CGGGGGCGCC CCTCCCGCAC 480
 CGCCTTAGGC TTCCTTTGAA GCCTCTGCGG TCAGGCCACC GCTTCCTGGG AAGCCCAAGC 540
 CAAGGCCAGG CCGAGTGGCC AACGGGAGGG GCCCGCGCGC GATTCTGGAG GAGGGCGGCG 600

GCCCCACAGG	TCTCCAGGGC	TGGCTAGCCG	GGCTCCTAGA	GCGGAGACTG	CCAAGGCCTT	660
CGGGTCCTGG	GCAGGAAGGA	TCCTGGCAGG	GAGGAGTTGC	TTGGGGGGTG	GGGGGGAAAG	720
GCTCCAGGCG	CGGTGGAGCT	CTGACCAGGA	GAATGCACAC	ACTCGGAGGG	GAGGAGGCGT	780
GTCAGCCCCA	AGCTAGCATC	CCACCCGGGG	AGCAGCGATG	TGGGGCGAAG	GTAGCCAGAG	840
CAAAAGAGCA	GGCACCAGGT	GACACGAAAC	AGAAGATTCC	GGGTAGAGCC	AGAACCCCAG	900
AAGTCCCATT	CAGGGAAGGT	GCGAGGCGAG	AACGAGTTAG	GTGGACCCTC	TCCAGGGGCA	960
GCCAAAGAAA	TCTAAAGAGA	ACCCGAAGGA	CTTGCCCGAA	AGAGAAACCG	AAAGCGGCGG	1020
TGGGCGGGAT	CGGTGGGCGG	GGCCTCCCTG	GTTTAAAGAGC	TTGATGCAGG	GGCGGGCAGC	1080
AGCAGAGAGA	ACTGCGGCCG	TGGCAGCGGC	ACGGCTCCCG	GCCCCGGAGC	ATGCGCGACA	1140
GCAGCCCCGG	AACCCCCAGC	CGCGGCGCCC	CGCGTCCCGC	CGCCAGGTGA	GCCGAGGCAG	1200
CTGCGAAGGA	GCAGGCGGGA	GGGGATGGGA	GGAAGGGGAG	CAGAGCCTGG	CAGGACTATC	1260
CTCGCAGACT	GCATGGCGGG	GTCGTGGATG	CTATGCCTCT	GGCGCCCGCC	CCACCGGCTG	1320
GCCCAGGCGG	CCCCTCGCGC	GCGCGGGGCG	CCGTCAGCCC	CTCCTCTCCG	GCCCTGAGCC	1380
CGGATCGTCC	GCCCCGGTTC	CAGTTCCCGG	CGTGGCCAGT	AGGCGGCAAC	CGCGAGGCGG	1440
CAAGCCACCC	AGCGGGGACG	GCCTGGAGTC	GGGCCCTCT	CCACGCCCCC	TTCTCCACGC	1500
GCGCGGGGAG	GCAGGGCTCC	ACCGCCAGTC	TGGAAGGGTT	CCACATACAG	GAACGGCCTA	1560
CTTCGCAGAT	GAGCCCACCG	AGGCTCAGGC	TCCGGGCGGA	TTCTGCGTGT	CACCCTCGCT	1620
CCTTGGGGTC	CGCTGGCCGG	CCTGTGCCAC	CCGGACGCCC	GGTTCACTGC	CTCTGTCTCC	1680
CCCATCAGCG	CAGCCCCGGA	CGGTATGGCC	CACCCCTCCA	GCTGGCCCCT	CGAGTAGGAT	1740
GGTAGCACGT	AACCAGGTGG	AAGCCGACAA	TGCGATCTCC	CCGGCATCAG	AGCCCCGACG	1800
GCGGCCAGAG	CCATCCTCGT	CCTCGTCTTC	GTCCTCGCCG	GCGGCCCCGG	CGCGTCCCCG	1860
GCCCTGCCCC	GTGGTCCCGG	CCCCGGCTCC	GGGCGACACT	CACTTCCGCA	CCTTCCGCTC	1920
CCACTCTGAT	TACCGGCGCA	TCACGCGGAC	CAGCGCTCTC	CTGGACGCCT	GCGGCTTCTA	1980
CTGGGGACCC	CTGAGCGTGC	ATGGGGCGCA	CGAACGGCTG	CGTTCCGAAC	CCGTGGGCAC	2040
CTTCTTGGTG	CGCGACAGTC	GCCAGCGGAA	CTGCTTCTTC	GCGCTCAGCG	TGAAGATGGC	2100
TTCGGGCCCC	ACGAGCATTC	GTGTGCACTT	CCAGGCCGGC	CGCTTCCACC	TGGACGGCAA	2160
CCGCGAGACC	TTGACTGCCC	TCTTCGAGCT	GCTGGAGCAC	TACGTGGCGG	CGCCGCGCCG	2220
CATGTTGGGG	GCCCCACTGC	GCCAGCGCCG	CGTGCGGCCG	CTGCAGGAGC	TGTGTCGCCA	2280

GCGCATCGTG GCCGCCGTGG GTCGCGAGAA CCTGGCACGC ATCCCTCTTA ACCCGGTACT 2340
 CCGTGACTAC CTGAGTTCCT TCCCCTTCCA GATCTGACCG GCTGCCGCCG TGCCCGCAGA 2400
 ATTAAGTGGG AGCGCCTTAT TATTTCTTAT TATTAATTAT TATTATTTTT CTGGAACCAC 2460
 GTGGGAGCCC TCCCCGCCTA GGTCGGAGGG AGTGGGTGTG GAGGGTGAGA TCCCTCCCAC 2520
 TTCTGGCTGG AGACCTTATC CCGCCTCTCG GGGGGCCTCC CCTCCTGGTG CTCCCTCCCG 2580
 GTCCCCCTGG TTGTAGCAGC TTGTGTCTGG GGCCAGGACC TGAACCTCCAC GCCTACCTCT 2640
 CCATGTTTAC ATGTTCCCAG TATCTTTGCA CAAACCAGGG GTGGGGGAGG GTCTCTGGCT 2700
 TCATTTTTCT GCTGTGCAGA ATATTCTATT TTATATTTTT ACATCCAGTT TAGATAATAA 2760
 ACTTTATTAT GAAAGTTTTT TTTTTTAAAG AAACAAAGAT TTCTAGA 2807

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Val	Ala	Arg	Asn	Gln	Val	Glu	Ala	Asp	Asn	Ala	Ile	Ser	Pro	Ala	1	5	10	15
Ser	Glu	Pro	Arg	Arg	Arg	Pro	Glu	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Ser	20	25	30	
Ser	Pro	Ala	Ala	Pro	Ala	Arg	Pro	Arg	Pro	Cys	Pro	Val	Val	Pro	Ala	35	40	45	
Pro	Ala	Pro	Gly	Asp	Thr	His	Phe	Arg	Thr	Phe	Arg	Ser	His	Ser	Asp	50	55	60	
Tyr	Arg	Arg	Ile	Thr	Arg	Thr	Ser	Ala	Leu	Leu	Asp	Ala	Cys	Gly	Phe	65	70	75	80
Tyr	Trp	Gly	Pro	Leu	Ser	Val	His	Gly	Ala	His	Glu	Arg	Leu	Arg	Ser	85	90	95	
Glu	Pro	Val	Gly	Thr	Phe	Leu	Val	Arg	Asp	Ser	Arg	Gln	Arg	Asn	Cys	100	105	110	

Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg
 115 120 125
 Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Asn Arg Glu Thr
 130 135 140
 Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg
 145 150 155 160
 Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln
 165 170 175
 Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu
 180 185 190
 Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe
 195 200 205
 Pro Phe Gln Ile
 210

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 263..1529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGAATTCGG GCGGGCTGTG TGAGTCTGTG AGTGAAGGC GCGCCGGCTC TTTTGTCTGA	60
GTGTGACCCG GTGGCTTTGT TCCAGGCATT CCGGTGATTT CCTCCGGGCA GTCCGCAGAA	120
GCCGCAGCGG CCGCCCGCGC TCTCTCTGCA GTCTCCACAC CCGGGAGAGC CTGAGCCCGC	180
GTCACGCCCC TCAGCCCCCG CTGAGTCCCT TCTCTGTTGT CGCGTCCGAA TCGAGTTCCC	240
GGAATCAGAC GGTGCCCCAT AG ATG GCC AGC TTT CCC CCG AGG GTT AAC GAG	292
Met Ala Ser Phe Pro Pro Arg Val Asn Glu	
1 5 10	
AAA GAG ATC GTG AGA TCA CGT ACT ATA GGG GAA CTC TTG GCT CCA GCA	340
Lys Glu Ile Val Arg Ser Arg Thr Ile Gly Glu Leu Leu Ala Pro Ala	
15 20 25	

GCT	CCT	TTT	GAC	AAG	AAA	TGT	GGT	GGT	GAG	AAC	TGG	ACG	GTT	GCT	TTT	388
Ala	Pro	Phe	Asp	Lys	Lys	Cys	Gly	Gly	Glu	Asn	Trp	Thr	Val	Ala	Phe	
			30					35					40			
GCT	CCT	GAT	GGT	TCC	TAC	TTT	GCG	TGG	TCA	CAA	GGA	TAT	CGC	ATA	GTG	436
Ala	Pro	Asp	Gly	Ser	Tyr	Phe	Ala	Trp	Ser	Gln	Gly	Tyr	Arg	Ile	Val	
		45					50					55				
AAG	CTT	GTC	CCG	TGG	TCC	CAG	TGC	CGT	AAG	AAC	TTT	CTT	TTG	CAT	GGT	484
Lys	Leu	Val	Pro	Trp	Ser	Gln	Cys	Arg	Lys	Asn	Phe	Leu	Leu	His	Gly	
	60					65					70					
TCC	AAA	AAT	GTT	ACC	AAT	TCA	AGC	TGT	CTA	AAA	TTG	GCA	AGA	CAA	AAC	532
Ser	Lys	Asn	Val	Thr	Asn	Ser	Ser	Cys	Leu	Lys	Leu	Ala	Arg	Gln	Asn	
	75				80					85					90	
AGT	AAT	GGT	GGT	CAG	AAA	AAC	AAG	CCT	CCT	GAG	CAC	GTT	ATA	GAC	TGT	580
Ser	Asn	Gly	Gly	Gln	Lys	Asn	Lys	Pro	Pro	Glu	His	Val	Ile	Asp	Cys	
				95				100						105		
GGA	GAC	ATA	GTC	TGG	AGT	CTT	GCT	TTT	GGG	TCT	TCA	GTT	CCA	GAA	AAA	628
Gly	Asp	Ile	Val	Trp	Ser	Leu	Ala	Phe	Gly	Ser	Ser	Val	Pro	Glu	Lys	
			110					115					120			
CAG	AGT	CGT	TGC	GTT	AAT	ATA	GAA	TGG	CAT	CGG	TTC	CGA	TTT	GGA	CAG	676
Gln	Ser	Arg	Cys	Val	Asn	Ile	Glu	Trp	His	Arg	Phe	Arg	Phe	Gly	Gln	
		125					130					135				
GAT	CAG	CTA	CTC	CTT	GCC	ACA	GGA	TTA	AAC	AAT	GGT	CGC	ATC	AAA	ATC	724
Asp	Gln	Leu	Leu	Leu	Ala	Thr	Gly	Leu	Asn	Asn	Gly	Arg	Ile	Lys	Ile	
	140					145					150					
TGG	GAT	GTA	TAT	ACA	GGA	AAA	CTC	CTC	CTT	AAT	TTG	GTA	GAC	CAC	ATT	772
Trp	Asp	Val	Tyr	Thr	Gly	Lys	Leu	Leu	Leu	Asn	Leu	Val	Asp	His	Ile	
	155				160					165					170	
GAA	ATG	GTT	AGA	GAT	TTA	ACT	TTT	GCT	CCA	GAT	GGG	AGC	TTA	CTC	CTT	820
Glu	Met	Val	Arg	Asp	Leu	Thr	Phe	Ala	Pro	Asp	Gly	Ser	Leu	Leu	Leu	
				175					180					185		
GTA	TCA	GCT	TCA	AGA	GAC	AAA	ACT	CTA	AGA	GTG	TGG	GAC	CTG	AAA	GAT	868
Val	Ser	Ala	Ser	Arg	Asp	Lys	Thr	Leu	Arg	Val	Trp	Asp	Leu	Lys	Asp	
			190					195					200			
GAT	GGA	AAC	ATG	GTG	AAA	GTA	TTG	CGG	GCA	CAT	CAG	AAT	TGG	GTG	TAC	916
Asp	Gly	Asn	Met	Val	Lys	Val	Leu	Arg	Ala	His	Gln	Asn	Trp	Val	Tyr	
		205					210					215				
AGT	TGT	GCA	TTC	TCT	CCC	GAC	TGT	TCT	ATG	CTG	TGT	TCA	GTG	GGC	GCC	964
Ser	Cys	Ala	Phe	Ser	Pro	Asp	Cys	Ser	Met	Leu	Cys	Ser	Val	Gly	Ala	
	220					225					230					
AGT	AAA	GCA	GTT	TTC	CTT	TGG	AAT	ATG	GAT	AAA	TAC	ACC	ATG	ATT	AGG	1012
Ser	Lys	Ala	Val	Phe	Leu	Trp	Asn	Met	Asp	Lys	Tyr	Thr	Met	Ile	Arg	
	235				240					245					250	

AAG CTG GAA GGT CAT CAC CAT GAT GTT GTA GCT TGT GAC TTT TCT CCT	1060
Lys Leu Glu Gly His His His Asp Val Val Ala Cys Asp Phe Ser Pro	
255 260 265	
GAT GGA GCA TTG CTA GCT ACT GCA TCC TAT GAC ACT CGT GTG TAT GTC	1108
Asp Gly Ala Leu Leu Ala Thr Ala Ser Tyr Asp Thr Arg Val Tyr Val	
270 275 280	
TGG GAT CCA CAC AAT GGA GAC CTT CTG ATG GAG TTT GGG CAC CTG TTT	1156
Trp Asp Pro His Asn Gly Asp Leu Leu Met Glu Phe Gly His Leu Phe	
285 290 295	
CCC TCG CCC ACT CCA ATA TTT GCT GGA GGA GCA AAT GAC CGA TGG GTG	1204
Pro Ser Pro Thr Pro Ile Phe Ala Gly Gly Ala Asn Asp Arg Trp Val	
300 305 310	
AGA GCT GTG TCT TTC AGT CAT GAT GGA CTG CAT GTT GCC AGC CTT GCT	1252
Arg Ala Val Ser Phe Ser His Asp Gly Leu His Val Ala Ser Leu Ala	
315 320 325 330	
GAT GAT AAA ATG GTG AGG TTC TGG AGA ATC GAT GAG GAT TGT CCG GTA	1300
Asp Asp Lys Met Val Arg Phe Trp Arg Ile Asp Glu Asp Cys Pro Val	
335 340 345	
CAA GTT GCA CCT TTG AGC AAT GGT CTT TGC TGT GCC TTT TCT ACT GAT	1348
Gln Val Ala Pro Leu Ser Asn Gly Leu Cys Cys Ala Phe Ser Thr Asp	
350 355 360	
GGC AGT GTT TTA GCT GCT GGG ACA CAT GAT GGA AGT GTG TAT TTT TGG	1396
Gly Ser Val Leu Ala Ala Gly Thr His Asp Gly Ser Val Tyr Phe Trp	
365 370 375	
GCC ACT CCA AGG CAA GTC CCT AGC CTT CAA CAT ATA TGT CGC ATG TCA	1444
Ala Thr Pro Arg Gln Val Pro Ser Leu Gln His Ile Cys Arg Met Ser	
380 385 390	
ATC CGA AGA GTG ATG TCC ACC CAA GAA GTC CAA AAA CTG CCT GTT CCT	1492
Ile Arg Arg Val Met Ser Thr Gln Glu Val Gln Lys Leu Pro Val Pro	
395 400 405 410	
TCC AAA ATA TTG GCG TTT CTC TCC TAC CGC GGT TAG A CTGAAGACTG	1539
Ser Lys Ile Leu Ala Phe Leu Ser Tyr Arg Gly *	
415 420	
CCTTTCCTGG TAGGCCTGCC AGACAGAGCG CCCTTTACAA GACACACCTC AAGCTTTACC	1599
TCGTGCCGAA TT	1611

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Ser	Phe	Pro	Pro	Arg	Val	Asn	Glu	Lys	Glu	Ile	Val	Arg	Ser
1				5					10					15	
Arg	Thr	Ile	Gly	Glu	Leu	Leu	Ala	Pro	Ala	Ala	Pro	Phe	Asp	Lys	Lys
			20					25					30		
Cys	Gly	Gly	Glu	Asn	Trp	Thr	Val	Ala	Phe	Ala	Pro	Asp	Gly	Ser	Tyr
		35					40					45			
Phe	Ala	Trp	Ser	Gln	Gly	Tyr	Arg	Ile	Val	Lys	Leu	Val	Pro	Trp	Ser
	50					55					60				
Gln	Cys	Arg	Lys	Asn	Phe	Leu	Leu	His	Gly	Ser	Lys	Asn	Val	Thr	Asn
65					70					75					80
Ser	Ser	Cys	Leu	Lys	Leu	Ala	Arg	Gln	Asn	Ser	Asn	Gly	Gly	Gln	Lys
				85					90					95	
Asn	Lys	Pro	Pro	Glu	His	Val	Ile	Asp	Cys	Gly	Asp	Ile	Val	Trp	Ser
			100					105					110		
Leu	Ala	Phe	Gly	Ser	Ser	Val	Pro	Glu	Lys	Gln	Ser	Arg	Cys	Val	Asn
		115					120					125			
Ile	Glu	Trp	His	Arg	Phe	Arg	Phe	Gly	Gln	Asp	Gln	Leu	Leu	Leu	Ala
	130					135					140				
Thr	Gly	Leu	Asn	Asn	Gly	Arg	Ile	Lys	Ile	Trp	Asp	Val	Tyr	Thr	Gly
145					150					155					160
Lys	Leu	Leu	Leu	Asn	Leu	Val	Asp	His	Ile	Glu	Met	Val	Arg	Asp	Leu
				165					170					175	
Thr	Phe	Ala	Pro	Asp	Gly	Ser	Leu	Leu	Leu	Val	Ser	Ala	Ser	Arg	Asp
			180					185					190		
Lys	Thr	Leu	Arg	Val	Trp	Asp	Leu	Lys	Asp	Asp	Gly	Asn	Met	Val	Lys
		195					200					205			
Val	Leu	Arg	Ala	His	Gln	Asn	Trp	Val	Tyr	Ser	Cys	Ala	Phe	Ser	Pro
	210					215					220				
Asp	Cys	Ser	Met	Leu	Cys	Ser	Val	Gly	Ala	Ser	Lys	Ala	Val	Phe	Leu
225					230					235					240
Trp	Asn	Met	Asp	Lys	Tyr	Thr	Met	Ile	Arg	Lys	Leu	Glu	Gly	His	His
				245					250					255	
His	Asp	Val	Val	Ala	Cys	Asp	Phe	Ser	Pro	Asp	Gly	Ala	Leu	Leu	Ala
			260					265					270		

Thr	Ala	Ser	Tyr	Asp	Thr	Arg	Val	Tyr	Val	Trp	Asp	Pro	His	Asn	Gly
		275					280					285			
Asp	Leu	Leu	Met	Glu	Phe	Gly	His	Leu	Phe	Pro	Ser	Pro	Thr	Pro	Ile
	290					295					300				
Phe	Ala	Gly	Gly	Ala	Asn	Asp	Arg	Trp	Val	Arg	Ala	Val	Ser	Phe	Ser
305					310					315					320
His	Asp	Gly	Leu	His	Val	Ala	Ser	Leu	Ala	Asp	Asp	Lys	Met	Val	Arg
				325					330					335	
Phe	Trp	Arg	Ile	Asp	Glu	Asp	Cys	Pro	Val	Gln	Val	Ala	Pro	Leu	Ser
			340					345					350		
Asn	Gly	Leu	Cys	Cys	Ala	Phe	Ser	Thr	Asp	Gly	Ser	Val	Leu	Ala	Ala
		355					360					365			
Gly	Thr	His	Asp	Gly	Ser	Val	Tyr	Phe	Trp	Ala	Thr	Pro	Arg	Gln	Val
	370					375					380				
Pro	Ser	Leu	Gln	His	Ile	Cys	Arg	Met	Ser	Ile	Arg	Arg	Val	Met	Ser
385					390					395					400
Thr	Gln	Glu	Val	Gln	Lys	Leu	Pro	Val	Pro	Ser	Lys	Ile	Leu	Ala	Phe
				405					410					415	
Leu	Ser	Tyr	Arg	Gly	*										
				420											

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGTCTTCCT	CCGCAGCGCG	AGGCTGGGTA	CAGGGTCTAT	TGTCTGTGGT	TGACTCCGTA	60
CTTTGGTCTG	AGGCCTTCGG	GAGCTTTCCC	GAGGCAGTTA	GCAGAAGCCG	CAGCGACCGC	120
CCCCGCCCCG	CTCCTCTGTC	CCTGGGCCCC	GGAGACAAAC	TTGGCGTCAC	GCCCTCAGCG	180
GTCGCCACTC	TCTTCTCTGT	TGTTGGGTCC	GCATCGTATT	CCCGGAATCA	GACGGTGCCC	240
CATAGATGGC	CAGCTTTCCC	CCGAGGGTCA	ACGAGAAAGA	GATCGTGAGA	TCACGTACTA	300
TAGGTGAACT	TTTAGCTCCT	GCAGCTCCTT	TTGACAAGAA	ATGTGGTCGT	GAAAATTGGA	360

CTGTTGCTTT	TGCTCCAGAT	GGTTCATACT	TTGCTTGGTC	ACAAGGACAT	CGCACAGTAA	420
AGCTTGTTCC	GTGGTCCCAG	TGCCTTCAGA	ACTTTCTCTT	GCATGGCACC	AAGAATGTTA	480
CCAATTCAAG	CAGTTTAAGA	TTGCCAAGAC	AAAATAGTGA	TGGTGGTCAG	AAAAATAAGC	540
CTCGTGACAT	ATTATAGACT	GTGGAGATAT	AGTCTGGAGT	CTTGCTTTTG	GGTCATCAGT	600
TCCAGAAAAA	CAGAGTCGCT	GTGTAAATAT	AGAATGGCAT	CGCTTCAGAT	TTGGACAAGA	660
TCAGCTACTT	CTTGCTACAG	GGTTGAACAA	TGGGCGTATC	AAAATATGGG	ATGTATATCA	720
GGAAACTCCT	CCTTAACTTG	GTAGATCATA	CTGAAGTGGT	CAGAGATTTA	ACTTTTGCTC	780
CAG						783

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTCTGTATGT	CTGAATGAAG	CTATAACATT	TGCCTTTTTTA	TTGCAGGTTT	TCCTTTGGAA	60
TATGGATAAA	TACACCATGA	TACGGAAACT	AGAAGGACAT	CACCATGATG	TGGTAGCTTG	120
TGACTTTTCT	CCTGATGGAG	CATTACTGGC	TACTGCATCT	TATGATACTC	GAGTATATAT	180
CTGGGATCCA	CATAATGGAG	ACATTCTGAT	GGAATTTGGG	CACCTGTTTC	CCCCACCTAC	240
TCCAATATTT	GCTGGAGGAG	CAAATGACCG	GTGGGTACGA	TCTGTATCTT	TTAGCCATGA	300
TGGACTGCAT	GTTGCAAGCC	TTGCTGATGA	TAAAATGGTG	AGGTTCTGGA	GAATTGATGA	360
GGATTATCCA	GTGCAAGTTG	CACCTTTGAG	CAATGGTCTT	TGCTGTGCCT	TCTCTACTGA	420
TGGCAGTGTT	TTAGCTGCTG	GGACACATGA	CGGAAGTGTG	TATTTTTGGG	CCACTCCACG	480
GCAGGTCCCT	AGCCTGCAAC	ATTTATGTCG	CATGTCAATC	CGAAGAGTGA	TGCCCACCCA	540
AGAAGTTCAG	GAGCTGCCGA	TTCTTCCAA	GCTTTTGGAG	TTTCTCTCGT	ATCGTATTTA	600
GAAGATTCTG	CCTTCCCTAG	TAGTAGGGAC	TGACAGAATA	CACCTAACAC	AAACCTCAAG	660
CTTTACTGAC	TTCAATTATC	TGTTTTTAAA	GACGTAGAAG	ATTTATTTAA	TTTGATATGT	720
TCTTGTA CTG	CATTTTGATC	AGTTGAGCTT	TTAAAATATT	ATTTATAGAC	AATAGAAGTA	780

TTTCTGAACA TATCAAATAT AAATTTTTTT AAAGATCTAA CTGTGAAAAC ATACATACCT	840
GTACATATTT AGATATAAGC TGCTATATGT TGAATGGACC CTTTTGCTTT TCTGATTTTT	900
AGTTCTGACA TGTATATATT GCTTCAGTAG AGCCACAATA TGTATCTTTG CTGTAAAGTG	960
CAAGGAAATT TTAAATTCTG GGACACTGAG TTAGATGGTA AATACTGACT TACGAAAGTT	1020
GAATTGGGTG AGGCGGGCAA ATCACCTGAG GTCAGCAGTT TGAGACTAGC CTGGCAAACA	1080
TGATGAAACC CTGTCTCTAC TAAAAATACA AAAAAAAAAA AA	1122

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 423..2030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGCACGAGC CGGGCTCCGT CCGGAGGAAG CGAGGCTGCG CCGCCGGCCC GGCAGGAGCG	60
GAGGACGGGA MGC GCGGGCG GTCGCGCTCG CCCTGTCGCT GACTGCGCTG CCCC GGCCCA	120
TCCTTGCCCTG GCCG CAGGTG CCCTGGATGA GGCCGCCGCG CGTGTCCCGG CCGCTGAGTG	180
TCCCCCGCGG TCGCCCGGCG CCTGCCCTCA AGCGGCCGCC TCTCCTTGCC CGGGTCCCCG	240
TTTTCCCCCG GCGCAGTCCT CCTCCGGTGG GCGCCTCCGC ACCTCGGCGC AGGCGGCACG	300
GCCCTCGGGC CGGGATGGAT CCGCCGGGAA GAGGAAGACA AGCCGGGGCG TTGAGCCCCT	360
GCGCACGGTG CCGCCGCGCG TAGTGGGAGC TTACTCGCAG TAGGCTCTCG CTCTTCTAAT	420
CA ATG GAT AAA GTG GGG AAA ATG TGG AAC AAC TTA AAA TAC AGA TGC	467
Met Asp Lys Val Gly Lys Met Trp Asn Asn Leu Lys Tyr Arg Cys	
1 5 10 15	
CAG AAT CTC TTC AGC CAC GAG GGA GGA AGC CGT AAT GAG AAC GTG GAG	515
Gln Asn Leu Phe Ser His Glu Gly Gly Ser Arg Asn Glu Asn Val Glu	
20 25 30	

ATG	AAC	CCC	AAC	AGA	TGT	CCG	TCT	GTC	AAA	GAG	AAA	AGC	ATC	AGT	CTG	563
Met	Asn	Pro	Asn	Arg	Cys	Pro	Ser	Val	Lys	Glu	Lys	Ser	Ile	Ser	Leu	
			35					40					45			
GGA	GAG	GCA	GCT	CCC	CAG	CAA	GAG	AGC	AGT	CCC	TTA	AGA	GAA	AAT	GTT	611
Gly	Glu	Ala	Ala	Pro	Gln	Gln	Glu	Ser	Ser	Pro	Leu	Arg	Glu	Asn	Val	
		50					55					60				
GCC	TTA	CAG	CTG	GGA	CTG	AGC	CCT	TCC	AAG	ACC	TTT	TCC	AGG	CGG	AAC	659
Ala	Leu	Gln	Leu	Gly	Leu	Ser	Pro	Ser	Lys	Thr	Phe	Ser	Arg	Arg	Asn	
	65					70					75					
CAA	AAC	TGT	GCC	GCA	GAG	ATC	CCT	CAA	GTG	GTT	GAA	ATC	AGC	ATC	GAG	707
Gln	Asn	Cys	Ala	Ala	Glu	Ile	Pro	Gln	Val	Val	Glu	Ile	Ser	Ile	Glu	
80					85				90						95	
AAA	GAC	AGT	GAC	TCG	GGT	GCC	ACC	CCA	GGA	AGG	AGG	CTT	GCA	CGG	AGA	755
Lys	Asp	Ser	Asp	Ser	Gly	Ala	Thr	Pro	Gly	Thr	Arg	Leu	Ala	Arg	Arg	
				100					105					110		
GAC	TCC	TAC	TCG	CGG	CAC	GCC	CCG	TGG	GGA	GGA	AAG	AAG	AAA	CAT	TCC	803
Asp	Ser	Tyr	Ser	Arg	His	Ala	Pro	Trp	Gly	Gly	Lys	Lys	Lys	His	Ser	
			115					120					125			
TGT	TCC	ACA	AAG	ACC	CAG	AGT	TCA	TTG	GAT	ACC	GAG	AAA	AAG	TTT	GGT	851
Cys	Ser	Thr	Lys	Thr	Gln	Ser	Ser	Leu	Asp	Thr	Glu	Lys	Lys	Phe	Gly	
		130					135					140				
AGA	ACT	CGA	AGC	GGC	CTT	CAG	AGG	CGA	GAG	CGG	CGC	TAT	GGA	GTC	AGC	899
Arg	Thr	Arg	Ser	Gly	Leu	Gln	Arg	Arg	Glu	Arg	Arg	Tyr	Gly	Val	Ser	
	145					150					155					
TCC	ATG	CAG	GAC	ATG	GAC	AGC	GTT	TCT	AGC	CGC	GCG	GTC	GGG	AGC	CGC	947
Ser	Met	Gln	Asp	Met	Asp	Ser	Val	Ser	Ser	Arg	Ala	Val	Gly	Ser	Arg	
160					165					170					175	
TCC	CTG	AGG	CAG	AGG	CTC	CAG	GAC	ACG	GTG	GGT	TTG	TGT	TTT	CCC	ATG	995
Ser	Leu	Arg	Gln	Arg	Leu	Gln	Asp	Thr	Val	Gly	Leu	Cys	Phe	Pro	Met	
			180						185					190		
AGA	ACT	TAC	AGC	AAG	CAG	TCA	AAG	CCA	CTC	TTT	TCC	AAT	AAA	AGA	AAA	1043
Arg	Thr	Tyr	Ser	Lys	Gln	Ser	Lys	Pro	Leu	Phe	Ser	Asn	Lys	Arg	Lys	
			195					200					205			
ATA	CAT	CTT	TCT	GAA	TTA	ATG	CTG	GAG	AAA	TGC	CCT	TTT	CCT	GCT	GGC	1091
Ile	His	Leu	Ser	Glu	Leu	Met	Leu	Glu	Lys	Cys	Pro	Phe	Pro	Ala	Gly	
	210					215						220				
TCG	GAT	TTA	GCA	CAA	AAG	TGG	CAT	TTG	ATT	AAA	CAG	CAT	ACC	GCC	CCT	1139
Ser	Asp	Leu	Ala	Gln	Lys	Trp	His	Leu	Ile	Lys	Gln	His	Thr	Ala	Pro	
	225					230					235					
GTG	AGC	CCA	CAC	TCA	ACA	TTT	TTT	GAT	ACA	TTT	GAT	CCA	TCA	CTG	GTG	1187
Val	Ser	Pro	His	Ser	Thr	Phe	Phe	Asp	Thr	Phe	Asp	Pro	Ser	Leu	Val	
240					245					250					255	

TCT	ACA	GAA	GAT	GAA	GAA	GAT	AGG	CTT	CGC	GAG	AGA	AGA	CGG	CTT	AGT	1235
Ser	Thr	Glu	Asp	Glu	Glu	Asp	Arg	Leu	Arg	Glu	Arg	Arg	Arg	Leu	Ser	
				260					265						270	
ATC	GAA	GAA	GGG	GTG	GAT	CCC	CCT	CCC	AAC	GCA	CAA	ATA	CAC	ACC	TTT	1283
Ile	Glu	Glu	Gly	Val	Asp	Pro	Pro	Pro	Asn	Ala	Gln	Ile	His	Thr	Phe	
			275					280						285		
GAA	GCT	ACT	GCA	CAG	GTC	AAC	CCA	TTG	TAT	AAG	CTG	GGA	CCA	AAG	TTA	1331
Glu	Ala	Thr	Ala	Gln	Val	Asn	Pro	Leu	Tyr	Lys	Leu	Gly	Pro	Lys	Leu	
		290					295					300				
GCT	CCT	GGG	ATG	ACA	GAG	ATA	AGT	GGA	GAT	GGT	TCT	GCA	ATT	CCA	CAA	1379
Ala	Pro	Gly	Met	Thr	Glu	Ile	Ser	Gly	Asp	Gly	Ser	Ala	Ile	Pro	Gln	
	305					310					315					
GCS	AAT	TGT	GAC	TCA	GAA	GAG	GAT	TCA	ACC	ACC	CTA	TGT	CTG	CAG	TCA	1427
Xaa	Asn	Cys	Asp	Ser	Glu	Glu	Asp	Ser	Thr	Thr	Leu	Cys	Leu	Gln	Ser	
320					325					330					335	
CGG	AGG	CAG	AAG	CAG	CGC	CAG	GTG	TCC	GGG	GAC	AGC	CAC	GCG	CAC	GTT	1475
Arg	Arg	Gln	Lys	Gln	Arg	Gln	Val	Ser	Gly	Asp	Ser	His	Ala	His	Val	
				340					345					350		
AGC	AGA	CAG	GGA	GCT	TGG	AAA	GTT	CAT	ACG	CAG	ATC	GAT	TAC	ATA	CAC	1523
Ser	Arg	Gln	Gly	Ala	Trp	Lys	Val	His	Thr	Gln	Ile	Asp	Tyr	Ile	His	
			355					360					365			
TGC	CTC	GTG	CCA	GAT	TTG	CTT	CAG	ATC	ACA	GGG	AAT	CCC	TGT	TAC	TGG	1571
Cys	Leu	Val	Pro	Asp	Leu	Leu	Gln	Ile	Thr	Gly	Asn	Pro	Cys	Tyr	Trp	
		370					375					380				
GGC	GTG	ATG	GAC	CGA	TAC	GAG	GCC	GAA	GCC	CTT	CTA	GAA	GGG	AAA	CCG	1619
Gly	Val	Met	Asp	Arg	Tyr	Glu	Ala	Glu	Ala	Leu	Leu	Glu	Gly	Lys	Pro	
	385					390					395					
GAA	GGC	ACG	TTC	TTG	CTC	AGG	GAC	TCT	GCA	CAG	GAG	GAC	TAC	CTC	TTC	1667
Glu	Gly	Thr	Phe	Ile	Leu	Arg	Asp	Ser	Ala	Gln	Glu	Asp	Tyr	Leu	Phe	
400				405						410					415	
TCT	GTG	AGC	TTC	CGC	CGC	TAC	AAC	AGG	TCT	CTG	CAC	GCC	CGG	ATC	GAG	1715
Ser	Val	Ser	Phe	Arg	Arg	Tyr	Asn	Arg	Ser	Leu	His	Ala	Arg	Ile	Glu	
				420					425					430		
CAG	TGG	AAC	CAC	AAC	TTC	AGC	TTC	GAT	GCC	CAT	GAC	CCC	TGC	GTG	TTT	1763
Gln	Trp	Asn	His	Asn	Phe	Ser	Phe	Asp	Ala	His	Asp	Pro	Cys	Val	Phe	
			435					440					445			
CAC	TCC	TCC	ACW	GTC	ACG	GGG	CTT	CTC	GAA	CAC	TAT	AAA	GAC	CCC	AGC	1811
His	Ser	Ser	Xaa	Val	Thr	Gly	Leu	Leu	Glu	His	Tyr	Lys	Asp	Pro	Ser	
		450					455					460				
TCT	TGC	ATG	TTT	TTT	GAA	CCG	TTG	CTA	ACG	ATA	TCA	CTG	AAT	AGA	ACT	1859
Ser	Cys	Met	Phe	Phe	Glu	Pro	Leu	Leu	Thr	Ile	Ser	Leu	Asn	Arg	Thr	
	465					470					475					

TTC CCT TTC AGC CTG CAG TAT ATC TGC CGC GCA GTG ATC TGC AGA TGC	1907
Phe Pro Phe Ser Leu Gln Tyr Ile Cys Arg Ala Val Ile Cys Arg Cys	
480 485 490 495	
ACT ACG TAT GAT GGG ATT GAC GGG CTC CCG CTA CCG TCG ATG TTA CAG	1955
Thr Thr Tyr Asp Gly Ile Asp Gly Leu Pro Leu Pro Ser Met Leu Gln	
500 505 510	
GAT TTT TTA AAA GAG TAT CAT TAT AAA CAA AAA GTT AGG GTT CGC TGG	2003
Asp Phe Leu Lys Glu Tyr His Tyr Lys Gln Lys Val Arg Val Arg Trp	
515 520 525	
TTA GAA CGA GAR CCA GTC AAA GCA AAG TAACTCCTGT CCCCAAAGGG	2050
Leu Glu Arg Xaa Pro Val Lys Ala Lys	
530 535	
CACTAACTAA GTCTGCTCCT CCCGTGCATC MGAAGTGCAC CCATAGGRAG GCAGTCAGCT	2110
GCTAGGATTT CCCACCCAGA ATGGGAGCTT AGTCATTAGC CTCTGCCCTA TGGGGTCCGC	2170
TGTTTCCTCAG ACAAAGGTGC CTAGGCACAG CAAGATGGCT TGCAGGTGTT CGGTGGGCTG	2230
TGACAACTGA GGGAGGCAAC TCTGGGGCAT TTGCTATGAA GAATTCTATT TCTTACCGAA	2290
GAACAAATTA TTAATATTGG ATGGGTATTT CAATAGTGTG ACTAATGTTT GAAATTATTT	2350
TTTCTAAGAA TTTTCTATA ACCTTCAGAA AAAGTAGTGA TGTTTGTAGT TACTATAAAT	2410
CAAGCTTTGA AAGTTCAAAA CAAACAAGTT AAATAAAAGA CTACCTTCCT TTTAGAGAAA	2470
ACAAATGCAA GTTTTCCGAG CCACAGGCAT TGTGCACTGT TAATGTTAGC TTGTTATCAG	2530
CTCCTTTCTC CTCC	2544

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Asp Lys Val Gly Lys Met Trp Asn Asn Leu Lys Tyr Arg Cys Gln	
1 5 10 15	
Asn Leu Phe Ser His Glu Gly Gly Ser Arg Asn Glu Asn Val Glu Met	
20 25 30	
Asn Pro Asn Arg Cys Pro Ser Val Lys Glu Lys Ser Ile Ser Leu Gly	
35 40 45	

Glu	Ala	Ala	Pro	Gln	Gln	Glu	Ser	Ser	Pro	Leu	Arg	Glu	Asn	Val	Ala	
	50					55					60					
Leu	Gln	Leu	Gly	Leu	Ser	Pro	Ser	Lys	Thr	Phe	Ser	Arg	Arg	Asn	Gln	
65					70					75					80	
Asn	Cys	Ala	Ala	Glu	Ile	Pro	Gln	Val	Val	Glu	Ile	Ser	Ile	Glu	Lys	
				85					90					95		
Asp	Ser	Asp	Ser	Gly	Ala	Thr	Pro	Gly	Thr	Arg	Leu	Ala	Arg	Arg	Asp	
			100					105					110			
Ser	Tyr	Ser	Arg	His	Ala	Pro	Trp	Gly	Gly	Lys	Lys	Lys	His	Ser	Cys	
		115					120					125				
Ser	Thr	Lys	Thr	Gln	Ser	Ser	Leu	Asp	Thr	Glu	Lys	Lys	Phe	Gly	Arg	
	130					135					140					
Thr	Arg	Ser	Gly	Leu	Gln	Arg	Arg	Glu	Arg	Arg	Tyr	Gly	Val	Ser	Ser	
145					150					155					160	
Met	Gln	Asp	Met	Asp	Ser	Val	Ser	Ser	Arg	Ala	Val	Gly	Ser	Arg	Ser	
				165					170					175		
Leu	Arg	Gln	Arg	Leu	Gln	Asp	Thr	Val	Gly	Leu	Cys	Phe	Pro	Met	Arg	
			180					185					190			
Thr	Tyr	Ser	Lys	Gln	Ser	Lys	Pro	Leu	Phe	Ser	Asn	Lys	Arg	Lys	Ile	
		195					200					205				
His	Leu	Ser	Glu	Leu	Met	Leu	Glu	Lys	Cys	Pro	Phe	Pro	Ala	Gly	Ser	
	210					215					220					
Asp	Leu	Ala	Gln	Lys	Trp	His	Leu	Ile	Lys	Gln	His	Thr	Ala	Pro	Val	
225					230					235					240	
Ser	Pro	His	Ser	Thr	Phe	Phe	Asp	Thr	Phe	Asp	Pro	Ser	Leu	Val	Ser	
				245					250					255		
Thr	Glu	Asp	Glu	Glu	Asp	Arg	Leu	Arg	Glu	Arg	Arg	Arg	Leu	Ser	Ile	
			260					265					270			
Glu	Glu	Gly	Val	Asp	Pro	Pro	Pro	Asn	Ala	Gln	Ile	His	Thr	Phe	Glu	
		275					280					285				
Ala	Thr	Ala	Gln	Val	Asn	Pro	Leu	Tyr	Lys	Leu	Gly	Pro	Lys	Leu	Ala	
	290					295					300					
Pro	Gly	Met	Thr	Glu	Ile	Ser	Gly	Asp	Gly	Ser	Ala	Ile	Pro	Gln	Xaa	
305					310					315					320	
Asn	Cys	Asp	Ser	Glu	Glu	Asp	Ser	Thr	Thr	Leu	Cys	Leu	Gln	Ser	Arg	
				325					330					335		

Arg	Gln	Lys	Gln	Arg	Gln	Val	Ser	Gly	Asp	Ser	His	Ala	His	Val	Ser
			340					345					350		
Arg	Gln	Gly	Ala	Trp	Lys	Val	His	Thr	Gln	Ile	Asp	Tyr	Ile	His	Cys
		355					360					365			
Leu	Val	Pro	Asp	Leu	Leu	Gln	Ile	Thr	Gly	Asn	Pro	Cys	Tyr	Trp	Gly
	370					375					380				
Val	Met	Asp	Arg	Tyr	Glu	Ala	Glu	Ala	Leu	Leu	Glu	Gly	Lys	Pro	Glu
385					390					395					400
Gly	Thr	Phe	Leu	Leu	Arg	Asp	Ser	Ala	Gln	Glu	Asp	Tyr	Leu	Phe	Ser
			405						410					415	
Val	Ser	Phe	Arg	Arg	Tyr	Asn	Arg	Ser	Leu	His	Ala	Arg	Ile	Glu	Gln
			420					425					430		
Trp	Asn	His	Asn	Phe	Ser	Phe	Asp	Ala	His	Asp	Pro	Cys	Val	Phe	His
	435						440					445			
Ser	Ser	Xaa	Val	Thr	Gly	Leu	Leu	Glu	His	Tyr	Lys	Asp	Pro	Ser	Ser
	450					455					460				
Cys	Met	Phe	Phe	Glu	Pro	Leu	Leu	Thr	Ile	Ser	Leu	Asn	Arg	Thr	Phe
465					470					475					480
Pro	Phe	Ser	Leu	Gln	Tyr	Ile	Cys	Arg	Ala	Val	Ile	Cys	Arg	Cys	Thr
				485					490					495	
Thr	Tyr	Asp	Gly	Ile	Asp	Gly	Leu	Pro	Leu	Pro	Ser	Met	Leu	Gln	Asp
			500					505					510		
Phe	Leu	Lys	Glu	Tyr	His	Tyr	Lys	Gln	Lys	Val	Arg	Val	Arg	Trp	Leu
		515					520					525			
Glu	Arg	Xaa	Pro	Val	Lys	Ala	Lys								
	530					535									

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATTAAACAG CATAACAGCTC CTGTGAGCCC ACATTCAACA TTTTTTGATA CTTTGATCCA

TCTTTGGTTT	CTACAGAAGA	TGAAGAAGAT	AGGCTTAGAG	AGAGAAGGCG	GCTTAGTATT	120
GAAGAAGGGG	TTGATCCCCC	TCCCAATGCA	CAAATACATA	CATTTGAAGC	TACTGCACAG	180
GTTAATCCAT	TATTAAACTG	GGACCAAAAT	TAGCTCCTGG	AATGACTGAA	ATAAGTGGGG	240
ACAGTTCTGC	AATTCCACAA	GCTAATTGTG	ACTCGGAAGA	GGATACAACC	ACCCTGTGTT	300
GCAGTCACGG	AGGCAGAAGC	AGCGTCAGAT	ATCTGGAGAC	AGGCATACCC	ATGTTAGCAG	360
ACAGGGAGCT	TGGAAAGTCC	ACACACAGAT	TGATTACATA	CCTGCTTCG	TGCCTGATTT	420
GCTTCAAATT	ACAGGGAATC	CCTGTTACTG	GGGAGTGATG	GACCGTTATG	AAGCAGAAGC	480
CCTTCTCGAA	GGGAAACCTG	AAGGCACGTT	TTTGCTCAGG	GACTCTGCGC	AAGAGGACTA	540
CTTCTTCTCT	GTGAGCTTCC	GCCGATACAA	CAGATCCCTG	CATGCCCCGAA	TTGAGCAGTG	600
GAATCACAAC	TTTAGTTTCG	ACGCCCATGA	CCCCTGTGTA	TTTCACTCCT	CCACTGTAAC	660
GGGACTTTTA	GAACATTATA	AAGATCCCAG	TTCGTGCATG	TTTTTTGAAC	CATTGCTTAC	720
TATATCACTA	AATAGGACTT	TCCCTTTTAG	CCTGCAGTAT	ATCTGTCGCG	CGGTAATCTG	780
CAGGTGCACT	ACGTATGATG	GAATTGATGG	GCTCCCTCTA	CCCTCAATGT	TACAGGATTT	840
TTTAAAAGAG	TATCATTATA	AACAAAAAGT	TAGAGTTCGC	TGGTTGGAAC	GAGAACCAGT	900
CAAGGCAAAG	TAAACTCTCC	GGTCCOCAA	GGGTGTTAAC	TAGGTCCGCT	TTCATGTGCA	960
TCAGACAGTA	CACCTATAGC	AAGCACACGT	AGCAGTGTTA	GGCTTTTTCA	TACAGTATGT	1020
AAGCTTAGTG	TTAGTATCTG	TCAGATGCTA	CCTGCTGTTA	CTTATTCAGA	TAAACATGGT	1080
GCCTATTGGA	ACAATAGCGG	ATAGAGCTAC	AGGTGTTTCA	TAAGACTACA	AAAACATTTT	1140
GCCTATTTTCG	CTAACAGTTT	GGTTTTTAAT	GGCTGTGGTA	TTTGAGTGAG	GCAACTCTGG	1200
GGCATTGTGT	ATGAAGAAAT	G				1221

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 116..1330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCACGAGGC GGTGGTGGCG GCGGCGGGCG CGGCCGCGGC GGGGCGGGCG CGGAATGAAG	60
GCCCACGGCC CTGGGGGCTG AGGCGCCCGC CGCCTGGGGC GGGCCGCGCG TCCTC ATG	118
	Met 1
GAG GCC GGA GAG GAG CCG CTG CTG CTG GCT GAA CTC AAG CCT GGG CGC	166
Glu Ala Gly Glu Glu Pro Leu Leu Leu Ala Glu Leu Lys Pro Gly Arg	
	5 10 15
CCC CAC CAG TTC GAC TGG AAG TCA AGC TGC GAG ACC TGG AGC GTG GCC	214
Pro His Gln Phe Asp Trp Lys Ser Ser Cys Glu Thr Trp Ser Val Ala	
	20 25 30
TTC TCG CCA GAC GGT TCC TGG TTC GCC TGG TCT CAA GGA CAC TGC GTG	262
Phe Ser Pro Asp Gly Ser Trp Phe Ala Trp Ser Gln Gly His Cys Val	
	35 40 45
GTC AAG CTG GTC CCC TGG CCC TTA GAG GAA CAG TTC ATC CCT AAA GGA	310
Val Lys Leu Val Pro Trp Pro Leu Glu Glu Gln Phe Ile Pro Lys Gly	
	50 55 60 65
TTC GAA GCC AAG AGC CGA AGC AGC AAG AAT GAC CCA AAA GGA CGG GGC	358
Phe Glu Ala Lys Ser Arg Ser Ser Lys Asn Asp Pro Lys Gly Arg Gly	
	70 75 80
AGT CTG AAG GAG AAG ACG CTG GAC TGT GGC CAG ATT GTG TGG GGG CTG	406
Ser Leu Lys Glu Lys Thr Leu Asp Cys Gly Gln Ile Val Trp Gly Leu	
	85 90 95
GCC TTC AGC CCG TGG CCC TCT CCA CCC AGC AGG AAA CTC TGG GCA CGT	454
Ala Phe Ser Pro Trp Pro Ser Pro Pro Ser Arg Lys Leu Trp Ala Arg	
	100 105 110
CAC CAT CCC CAG GCG CCT GAT GTT TCT TGC CTG ATC CTG GCC ACA GGT	502
His His Pro Gln Ala Pro Asp Val Ser Cys Leu Ile Leu Ala Thr Gly	
	115 120 125
CTC AAC GAT GGG CAG ATC AAG ATT TGG GAG GTA CAG ACA GGC CTC CTG	550
Leu Asn Asp Gly Gln Ile Lys Ile Trp Glu Val Gln Thr Gly Leu Leu	
	130 135 140 145
CTT CTG AAT CTT TCT GGC CAC CAA GAC GTC GTG AGA GAT CTG AGC TTC	598
Leu Leu Asn Leu Ser Gly His Gln Asp Val Val Arg Asp Leu Ser Phe	
	150 155 160
ACG CCC AGC GGC AGT TTG ATT TTG GTC TCT GCA TCC CGG GAT AAG ACA	646
Thr Pro Ser Gly Ser Leu Ile Leu Val Ser Ala Ser Arg Asp Lys Thr	
	165 170 175

CTT	CGA	ATT	TGG	GAC	CTG	AAT	AAA	CAC	GGT	AAG	CAG	ATC	CAG	GTG	TTA	694
Leu	Arg	Ile	Trp	Asp	Leu	Asn	Lys	His	Gly	Lys	Gln	Ile	Gln	Val	Leu	
		180					185					190				
TCC	GGC	CAT	CTG	CAG	TGG	GTT	TAC	TGC	TGC	TCC	ATC	TCC	CCT	GAC	TGT	742
Ser	Gly	His	Leu	Gln	Trp	Val	Tyr	Cys	Cys	Ser	Ile	Ser	Pro	Asp	Cys	
	195					200					205					
AGC	ATG	CTG	TGC	TCT	GCA	GCT	GGG	GAG	AAG	TCG	GTC	TTT	CTG	TGG	AGC	790
Ser	Met	Leu	Cys	Ser	Ala	Ala	Gly	Glu	Lys	Ser	Val	Phe	Leu	Trp	Ser	
210					215					220					225	
ATG	CGG	TCC	TAC	ACA	CTA	ATC	CGG	AAA	CTA	GAA	GGC	CAC	CAA	AGC	AGT	838
Met	Arg	Ser	Tyr	Thr	Leu	Ile	Arg	Lys	Leu	Glu	Gly	His	Gln	Ser	Ser	
				230					235					240		
GTT	GTC	TCC	TGT	GAT	TTC	TCT	CCT	GAT	TCA	GCC	TTG	CTT	GTC	ACA	GCT	886
Val	Val	Ser	Cys	Asp	Phe	Ser	Pro	Asp	Ser	Ala	Leu	Leu	Val	Thr	Ala	
			245					250					255			
TCG	TAT	GAC	ACC	AGT	GTG	ATT	ATG	TGG	GAC	CCC	TAC	ACC	GGC	GCG	AGG	934
Ser	Tyr	Asp	Thr	Ser	Val	Ile	Met	Trp	Asp	Pro	Tyr	Thr	Gly	Ala	Arg	
		260					265					270				
CTG	AGG	TCA	CTT	CAT	CAC	ACA	CAA	CTT	GAA	CCC	ACC	ATG	GAT	GAC	AGT	982
Leu	Arg	Ser	Leu	His	His	Thr	Gln	Leu	Glu	Pro	Thr	Met	Asp	Asp	Ser	
	275					280					285					
GAC	GTC	CAC	ATG	AGC	TCC	CTG	AGG	TCC	GTG	TGC	TTC	TCA	CCT	GAA	GGC	1030
Asp	Val	His	Met	Ser	Ser	Leu	Arg	Ser	Val	Cys	Phe	Ser	Pro	Glu	Gly	
290					295					300					305	
TTG	TAT	CTC	GCT	ACG	GTG	GCA	GAT	GAC	AGG	CTG	CTC	AGG	ATC	TGG	GCT	1078
Leu	Tyr	Leu	Ala	Thr	Val	Ala	Asp	Asp	Arg	Leu	Leu	Arg	Ile	Trp	Ala	
				310					315					320		
CTG	GAA	CTG	AAG	GCT	CCG	GTT	GCC	TTT	GCT	CCG	ATG	ACC	AAT	GGT	CTT	1126
Leu	Glu	Leu	Lys	Ala	Pro	Val	Ala	Phe	Ala	Pro	Met	Thr	Asn	Gly	Leu	
			325					330					335			
TGC	TGC	ACG	TTC	TTC	CCA	CAC	GGT	GGA	ATT	ATT	GCC	ACA	GGG	ACG	AGA	1174
Cys	Cys	Thr	Phe	Phe	Pro	His	Gly	Gly	Ile	Ile	Ala	Thr	Gly	Thr	Arg	
		340					345					350				
GAT	GGC	CAT	GTC	CAG	TTC	TGG	ACA	GCT	CCC	CGG	GTC	CTG	TCC	TCA	CTG	1222
Asp	Gly	His	Val	Gln	Phe	Trp	Thr	Ala	Pro	Arg	Val	Leu	Ser	Ser	Leu	
	355					360					365					
AAG	CAC	TTA	TGC	AGG	AAA	GCC	CTC	CGA	AGT	TTC	CTG	ACA	ACG	TAT	CAA	1270
Lys	His	Leu	Cys	Arg	Lys	Ala	Leu	Arg	Ser	Phe	Leu	Thr	Thr	Tyr	Gln	
370					375					380					385	
GTC	CTA	GCA	CTG	CCA	ATC	CCC	AAG	AAG	ATG	AAA	GAG	TTC	CTC	ACA	TAC	1318
Val	Leu	Ala	Leu	Pro	Ile	Pro	Lys	Lys	Met	Lys	Glu	Phe	Leu	Thr	Tyr	
				390					395					400		

AGG ACT TTC TAGCAGTGCC GGCTCCCCCA CCTCCTGCAG CAGCAGCAGT	1367
Arg Thr Phe	
405	
ACAAGGGACT GGCTAGGATG GAGTCAGGCA GCTCACACTG GACCAGTGTG GACCTTCCTT	1427
CCTCCCATGG CATGTGCAAG TAGGTCTGCG TGACCCCACT TCTGTGGTGC CGGCCTTACC	1487
TCGTCTTCAT CCGTGGTGAG CAGCCTTCGT CAGTCTAGTT GTGTTGAAGC CAAGTGCAGT	1547
TGTGGATGTT GCTGGGGTAA TAAAGGCAAG CGGGCTCCAG AGCCTCTCTG GTGGCGGCCA	1607
AGCCACACTC CCTTAACTGG GAAGTACCTG CCACGTAGGG CATTCTCTGCT GCCTATTTCC	1667
AGCCAGCGGC TGCATGGTTT GAAGTTCCTC CGTTGTGGTC AGAAGAACTC TGGTGTGTTGG	1727
TTCCCTGCTC AGCTGCGCGT GGAAGTGGGCT GAGCTCCTCA CCATACACTA GTGCCGGCTT	1787
TTGTTTCCTG TAAACAGTGG TTGCATGTGT AGAGAAGTAA CAAGCGAGTA TTCAGATCAT	1847
ACGAGGAGGC GTTCCTCGGT GCATGACGGT CAGATGGCCA TTTATCAGCA TATTTATTTG	1907
TATTTTCTCA GCACATAGTA AGGTACAACGT GTGTTTCTC AATTGTCTCG AAAAAACAGA	1967
GTTCTTAAGT GGCCCAAGTTG TGGAGCCAAG TCTAAGTCGT GTGGAGTCAG TGCTGACATC	2027
ACTGGCTTGT GCTGTCTGTC ACATGTGTTT GTCTCTGCTG CTTGACCTCA TGGGATGTAC	2087
CCTCCAGTTC AACTGCCCAA AACAGACAGC CCCTTCCAAG CACCGTTCTT TGACAGCGGT	2147
AGCAGCTACC TATTCAAGAC GCCTCACACA AAATCTGCCT TAGAAAGTTA ATATATTTTA	2207
AATTATTTTA AAAGAAACTC AACATCTTAT TCTTTGGCCT TTCTTAATTG ATGCTTTATG	2267
GAGGCAGTGT TAACATTGTA CAGTGTATGC ATAGAGGAGT CTCCTCTATT TGAAGAACAA	2327
TGCAAAATGA GGCTTTTCAAT GAAGGGAAAA AAAAAAAAAA AA	2369

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 404 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Glu	Ala	Gly	Glu	Glu	Pro	Leu	Leu	Leu	Ala	Glu	Leu	Lys	Pro	Gly
1				5					10					15	
Arg	Pro	His	Gln	Phe	Asp	Trp	Lys	Ser	Ser	Cys	Glu	Thr	Trp	Ser	Val
			20					25					30		

Ala	Phe	Ser	Pro	Asp	Gly	Ser	Trp	Phe	Ala	Trp	Ser	Gln	Gly	His	Cys
		35					40					45			
Val	Val	Lys	Leu	Val	Pro	Trp	Pro	Leu	Glu	Glu	Gln	Phe	Ile	Pro	Lys
	50					55					60				
Gly	Phe	Glu	Ala	Lys	Ser	Arg	Ser	Ser	Lys	Asn	Asp	Pro	Lys	Gly	Arg
65					70					75					80
Gly	Ser	Leu	Lys	Glu	Lys	Thr	Leu	Asp	Cys	Gly	Gln	Ile	Val	Trp	Gly
				85					90					95	
Leu	Ala	Phe	Ser	Pro	Trp	Pro	Ser	Pro	Pro	Ser	Arg	Lys	Leu	Trp	Ala
			100					105					110		
Arg	His	His	Pro	Gln	Ala	Pro	Asp	Val	Ser	Cys	Leu	Ile	Leu	Ala	Thr
		115					120					125			
Gly	Leu	Asn	Asp	Gly	Gln	Ile	Lys	Ile	Trp	Glu	Val	Gln	Thr	Gly	Leu
130						135					140				
Leu	Leu	Leu	Asn	Leu	Ser	Gly	His	Gln	Asp	Val	Val	Arg	Asp	Leu	Ser
145					150					155					160
Phe	Thr	Pro	Ser	Gly	Ser	Leu	Ile	Leu	Val	Ser	Ala	Ser	Arg	Asp	Lys
				165					170					175	
Thr	Leu	Arg	Ile	Trp	Asp	Leu	Asn	Lys	His	Gly	Lys	Gln	Ile	Gln	Val
			180					185					190		
Leu	Ser	Gly	His	Leu	Gln	Trp	Val	Tyr	Cys	Cys	Ser	Ile	Ser	Pro	Asp
		195					200					205			
Cys	Ser	Met	Leu	Cys	Ser	Ala	Ala	Gly	Glu	Lys	Ser	Val	Phe	Leu	Trp
	210					215					220				
Ser	Met	Arg	Ser	Tyr	Thr	Leu	Ile	Arg	Lys	Leu	Glu	Gly	His	Gln	Ser
225					230					235					240
Ser	Val	Val	Ser	Cys	Asp	Phe	Ser	Pro	Asp	Ser	Ala	Leu	Leu	Val	Thr
				245					250					255	
Ala	Ser	Tyr	Asp	Thr	Ser	Val	Ile	Met	Trp	Asp	Pro	Tyr	Thr	Gly	Ala
			260					265					270		
Arg	Leu	Arg	Ser	Leu	His	His	Thr	Gln	Leu	Glu	Pro	Thr	Met	Asp	Asp
		275					280					285			
Ser	Asp	Val	His	Met	Ser	Ser	Leu	Arg	Ser	Val	Cys	Phe	Ser	Pro	Glu
	290					295					300				
Gly	Leu	Tyr	Leu	Ala	Thr	Val	Ala	Asp	Asp	Arg	Leu	Leu	Arg	Ile	Trp
305					310					315					320

Ala Leu Glu Leu Lys Ala Pro Val Ala Phe Ala Pro Met Thr Asn Gly
 325 330 335
 Leu Cys Cys Thr Phe Phe Pro His Gly Gly Ile Ile Ala Thr Gly Thr
 340 345 350
 Arg Asp Gly His Val Gln Phe Trp Thr Ala Pro Arg Val Leu Ser Ser
 355 360 365
 Leu Lys His Leu Cys Arg Lys Ala Leu Arg Ser Phe Leu Thr Thr Tyr
 370 375 380
 Gln Val Leu Ala Leu Pro Ile Pro Lys Lys Met Lys Glu Phe Leu Thr
 385 390 395 400
 Tyr Arg Thr Phe

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACACTGCAT CGTCAAAGT ATCCCCTGGC CGTTGGAGGA GCAGTTCATC CCTAAAGGGT	60
TTGAAGCCAA AAGCCGAAGT AGCAAAAATG AGACGAAAGG GCGGGGCAGC CCAAAGAGA	120
AGACGCTGGA CTGTGGTCAG ATTGTCTGGG GGCTGGCCTT CAGCCTGTGC TTTCCCCACC	180
CAGCAGGAAG CTCTGGGCAC GCCACCACCC CCAAGTGCCC GATGTCTCTT GCCTGGTTCT	240
TGCTACGGGA CTCAACGATG GGCAGATCAA GATCTGGGAG GTGCAGACAG GGCTCCTGCT	300
TTTGAATCTT TCCGGCCACC AAGATGTCGT GAGAGATCTG AGCTTCACAC CCAGTGGCAG	360
TTTGATTTTG GTCTCGGCGT CACGGGATAA GACTCTTCGC ATCTGGGACC TGAATAACA	420
CGGTAAACAG ATTCAAGTGT TATCGGGCCA CCTGCAGTGG GTTTACTGCT GTTCCATCTC	480
CCCAGACTGC AGCATGCTGT GCTCTGCAGC TGGAGAGAAG TCGGTCTTTC TATGGAGCAT	540
GAGGTCCTAC ACGTTAATTC GGAAGCTAGA GGGCCATCAA AGCAGTGTTG TCTCTTGTTA	600
CTTCTCCCCC GACTCTGCCC TGCTTGTCAC GGCTTCTTAC GATACCAATG TGATTATGTG	660
GGACCCCTAC ACCGGCGAAA GGCTGAGGTC ACTCCACCAC ACCCAGGTTG ACCCCGCCAT	720

GGATGACAGT GACGTCCACA TTAGCTCACT GAGATCTGTG TGCTTCTCTC CAGAAGGCTT	780
GTACCTTGCC ACGGTGGCAG ATGACAGACT CCTCAGGATC TGGGCCCTGG AACTGAAAAC	840
TCCCATTGCA TTTGCTCCTA TGACCAATGG GCTTTGCTGG CACATTTTTT CCACATGGTG	900
GAGTCATTGC CACAGGGACA AGAGATGGCC ACGTCCAGTT CTGGACAGCT CCTAGGGTCC	960
TGTCCTCACT GAAGCACTTA TGCCGGAAAG CCCTTCGAAG TTTCTAACA ACTTACCAAG	1020
TCCTAGCACT GCCAATCCCC AAGAAAATGA AAGAGTTCCT CACATACAGG ACTTTTAAAG	1080
CAACACCACA TCTTGTGCTT CTTTGTAGCA GGGTAAATCG TCCTGTCAAA GGGAGTTGCT	1140
GGAATAATGG GCCAAACATC TGGTCTTGCA TTGAAATAGC ATTTCTTTGG GATTGTGAAT	1200
AGAATGTAGC AAAACCAGAT TCCAGTGTAC TAGTCATCGA TTTTTC	1246

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACCATGGTTC CAAGTCCTCT CCCCTGTGGT CAAGTTGCCC GAATGTTGGG CCAAGTGCC	60
TTTTCCTCCT TGGGCCTCCC CTCTGACCT GCAGGACAGT TTTCCGGAGC CCATTTGGTA	120
TGAGGTATTA ATTAGCCTTA ACTAAATTAC AGGGGACTCA GAGGCCGTGC TCCTGACCGA	180
TCCAGACACT ATTTTTTTTT TTTTTTTTTA ACAATGGTGT GCATGTGCAG GAAATGACAA	240
ATTTGTATGT CAGATTATAC AAGGATGTAT TCTTAAACCG CATGACTATT CAGATGGCTA	300
CTGAGTTATC AGTGGCCATT TATTAGCATC ATATTTATTT GTATTTTCTC AACAGATGTT	360
AAGGTACAAC TGTGTTTTTC TCGATTATCT AAAAACCATA GTAATAAAT TGAAAAAAAAA	420
AA	422

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2019 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCACGAGGC	GGGGTCAGGG	CGGAGGCTGA	GGACCAAGTA	GGCATGGCGG	AGGGCGGGAC	60
CGGCCCCGAT	GGACGGGCCG	GCCCGGGACC	CGCAGGTCCT	AATCTGAAGG	AGTGGCTGAG	120
GGAGCAGTTC	TGTGACCATC	CACTGGAGCA	CTGTGACGAT	ACAAGACTCC	ATGATGCAGC	180
CTATGTAGGG	GACCTCCAGA	CCCTCAGGAA	CCTACTGCAA	GAGGAGAGCT	ACCGGAGCCG	240
CATCAATGAG	AAGTCTGTCT	GGTGCTGCGG	CTGGCTTCCC	TGCACACCAC	TGAGGATCGC	300
AGCCACTGCA	GGCCATGGGA	ACTGTGTGGA	CTTCCTCATA	CGCAAAGGGG	CCGAGGTGGA	360
CCTGGTGGAT	GTCAAGGGGC	AGACTGCCCT	GTATGTGGCT	GTAAGTGAACG	GGCACTTGGA	420
GAGCACTGAG	ATCCTTTTGG	AAGCTGGTGC	TGATCCCAAC	GGCAGCCGGC	ACCACCGCAG	480
CACTCCTGTG	TACCATGCCT	YTCGTGTGGG	TAGGGACGAC	ATCCTGAAGG	CTCTTATCAG	540
GTATGGGGCA	GATGTTGATG	TCAACCATCA	TCTGAATTCT	GACACCCGGC	CCCCTTTTTC	600
ACGGCGGCTA	ACCTCCTTGG	TGGTCTGTCC	TCTATACATC	AGTGCTGCCT	ACCATAACCT	660
TCAGTGCTTC	AGGCTGCTCT	TGCAGGCTGG	GGCAAATCCT	GACTTCAATT	GCAATGGCCC	720
TGTCAACACC	CAGGAGTTCT	ACAGGGGATC	CCCTGGGTGT	GTCATGGATG	CTGTCCTGCG	780
CCATGGCTGT	GAAGCAGCCT	TCGTGAGTCT	GTTGGTAGAG	TTTGGAGCCA	ACCTGAACCT	840
GGTGAAGTGG	GAATCCCTGG	GCCCAGAGGC	AAGAGGCAGA	AGAAAGATGG	ATCCTGAGGC	900
CTTGCAGGTC	TTTAAAGAGG	CCAGAAGTAT	TCCCAGGACC	TTGCTGAGTT	TGTGCCGGGT	960
GGCTGTGAGA	AGAGCTCTTG	GCAAATACCG	ACTGCATCTG	GTTCCCTCGC	TGCCGCTGCC	1020
AGACCCCAT	AAGAAGTTTT	TGCTTTATGA	GTAAGCATTC	CATGCAGTGC	TGACTGCAAT	1080
GTGGAAGCCG	ATCACCTGCA	GTGAAAACCTG	ACACAGACTC	TGGCATCCTG	GGAACCATGG	1140
CCTGTGCTGC	CAGCTTGATC	CTTGGCTGTC	AGTGAAGAAA	AAACGGCTGT	GTTCTCTTGG	1200
ACTGTGATTC	TATCTCAGGT	GCTTGGGCCA	TCGAACGCTC	CTTGAGTCAT	TGTCAACTGA	1260
GAGGCACATA	CAAACTTAAT	TTTGTTCCTC	TTCAGTCTCT	CTGTTTTGGA	TTCTTCCTGG	1320
CAATGTGTGC	AGCATGGGCT	GAGCCTGGTG	ATTGCCCTAG	TGGGGAAGGC	TTTTTTCTCC	1380
AGGCTATGCA	TCTATTTATG	TTCCTACTTT	GCAATTTATT	GTTCTTTTAA	GGCTTGATAT	1440

CAAAACAGAA AGAGGTTTGT TAAGAAAAGA TATAGGGAGA AAGGAATTCC GGTTCCGTGC	1500
ACTTGCTAGC CTGCTTTCCT TGCCTGGGTT TGTCTGTCTA TGCTGCCTGG TGCACATCCC	1560
TTCTCTTTGC TGCCACTGTT CTATTTTGGG AGTTGTCTTC CGTCTAAGAT GGCTTCTGGG	1620
GTTCTATCTT ATTGCACAGA GGTCCCAGAA CAGTGTTTCAT AGGGCACCAT CTGCTCTGCC	1680
AAGGGTTTTC TGATGTCTTA CCCTGGGGAT CTTCAGACAG TGGTTACCTT TAGGAGACCC	1740
ACCTGGAAct AACCATTAAG TGA CTGCCCA CATT CAGATC AGGGACCATC TTAATAGTAC	1800
TC ACTGCCAG TCCTCACAAG AGAAGATGAC ACGGGTGCTC TCTTCAGACA CTCCCATA CA	1860
GGAAGTTGGA AAATGTCTTG GTCACCTGGG TTGTTCCCAG GCTACA ACTT CTTGGTGTTC	1920
CACTAARACC AGRATATCCT AGTTTTTTGG GTTGACTGTT CCCTCCCCAC TTTCCTTGAA	1980
NCCCAATGCC CNTTTGTKTN GGTGCTTCC CTAAAAKTT	2019

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala	Arg	Gly	Gly	Val	Arg	Ala	Glu	Ala	Glu	Asp	Gln	Val	Gly	Met	Ala
1				5					10					15	
Glu	Gly	Gly	Thr	Gly	Pro	Asp	Gly	Arg	Ala	Gly	Pro	Gly	Pro	Ala	Gly
			20					25					30		
Pro	Asn	Leu	Lys	Glu	Trp	Leu	Arg	Glu	Gln	Phe	Cys	Asp	His	Pro	Leu
		35					40					45			
Glu	His	Cys	Asp	Asp	Thr	Arg	Leu	His	Asp	Ala	Ala	Tyr	Val	Gly	Asp
	50					55					60				
Leu	Gln	Thr	Leu	Arg	Asn	Leu	Leu	Gln	Glu	Glu	Ser	Tyr	Arg	Ser	Arg
65					70					75					80
Ile	Asn	Glu	Lys	Ser	Val	Trp	Cys	Cys	Gly	Trp	Leu	Pro	Cys	Thr	Pro
			85						90					95	
Leu	Arg	Ile	Ala	Ala	Thr	Ala	Gly	His	Gly	Asn	Cys	Val	Asp	Phe	Leu
			100					105					110		

Ile	Arg	Lys	Gly	Ala	Glu	Val	Asp	Leu	Val	Asp	Val	Lys	Gly	Gln	Thr
		115					120					125			
Ala	Leu	Tyr	Val	Ala	Val	Val	Asn	Gly	His	Leu	Glu	Ser	Thr	Glu	Ile
		130				135					140				
Leu	Leu	Glu	Ala	Gly	Ala	Asp	Pro	Asn	Gly	Ser	Arg	His	His	Arg	Ser
145					150					155					160
Thr	Pro	Val	Tyr	His	Ala	Xaa	Arg	Val	Gly	Arg	Asp	Asp	Ile	Leu	Lys
				165					170					175	
Ala	Leu	Ile	Arg	Tyr	Gly	Ala	Asp	Val	Asp	Val	Asn	His	His	Leu	Asn
			180					185					190		
Ser	Asp	Thr	Arg	Pro	Pro	Phe	Ser	Arg	Arg	Leu	Thr	Ser	Leu	Val	Val
		195					200					205			
Cys	Pro	Leu	Tyr	Ile	Ser	Ala	Ala	Tyr	His	Asn	Leu	Gln	Cys	Phe	Arg
	210					215					220				
Leu	Leu	Leu	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Phe	Asn	Cys	Asn	Gly	Pro
225					230					235					240
Val	Asn	Thr	Gln	Glu	Phe	Tyr	Arg	Gly	Ser	Pro	Gly	Cys	Val	Met	Asp
				245					250					255	
Ala	Val	Leu	Arg	His	Gly	Cys	Glu	Ala	Ala	Phe	Val	Ser	Leu	Leu	Val
			260					265					270		
Glu	Phe	Gly	Ala	Asn	Leu	Asn	Leu	Val	Lys	Trp	Glu	Ser	Leu	Gly	Pro
	275						280					285			
Glu	Ala	Arg	Gly	Arg	Arg	Lys	Met	Asp	Pro	Glu	Ala	Leu	Gln	Val	Phe
	290					295					300				
Lys	Glu	Ala	Arg	Ser	Ile	Pro	Arg	Thr	Leu	Leu	Ser	Leu	Cys	Arg	Val
305					310					315					320
Ala	Val	Arg	Arg	Ala	Leu	Gly	Lys	Tyr	Arg	Leu	His	Leu	Val	Pro	Ser
				325					330					335	
Leu	Pro	Leu	Pro	Asp	Pro	Ile	Lys	Lys	Phe	Leu	Leu	Tyr	Glu		
			340					345					350		

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCATCCATGG	CGGAGGGCGG	CAGCACGACG	GGCGGGCAGG	GCCGGGCTCC	GCAGGTCGTA	60
ATCTGAAGGA	GTGGCTGAGG	GAGCAATTTT	GTGATCATCC	GCTGGAGCAC	TGTGAGGACA	120
CGAGGCTCCA	TGATGCAGCT	TACGTCGGGG	ACCTCCAGAC	CCTCAGGAGC	CTATTGCAAG	180
AGGAGAGCTA	CCGAGCCGC	ATCAACGAGA	AGTCTGTCTG	GTGCTGTGGC	TGGCTCCCCT	240
GCACACCGTT	GCGAATCGCG	GCCACTGCAG	GCCATGGGAG	CTGTGTGGAC	TTCCTCATCC	300
GGAAGGGGGC	CGAGGTGGAT	CTGGTGGACG	TAAAAGGACA	GACGGCCCTG	TATGTGGCTG	360
TGGTGAACGG	GCACCTAGAG	AGTACCCAGA	TCCTTCTCGA	AGCTGGCGCG	GACCCCAAC	419

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGGAAGAAG	AAAAGTGGAC	CCTGAGGCTT	TGCAGGTCTT	TAAAGAGGCC	AGAAGTGTTT	60
CCAGAACCTT	GCTGTGTCTG	TGCCGTGTGG	CTGTGAGAAG	AGCTCTTGGC	AAAACCGGCT	120
TCATCTGATT	CCTTCGCTGC	CTCTGCCAGA	CCCCATAAAG	AAGTTTCTAC	TCCATGAGTA	180
GACTCCAAGT	GCTGCGGTTG	ATTCCAGTGA	GGGAGAAAGT	GATCTGCAGG	GAGGTGGACA	240
CCGAGCCCTG	AGTGCTGTGC	TGCTGCTGGT	CTCCTGATGG	CTGTTGCTGC	AGAAGATGTC	300
CTCGTAGACT	GTCATTGCTC	CTCAGGTGCC	TGGGCCGCTG	AACAGTCCTT	GGGTCATTGT	360
CAGCTGAGAG	GCTTATACTA	AAGTTATTAT	TGTTTTTCCC	AAGTTCTCTG	TTCTGGATTT	420
TCAGTTGCAT	ATTAATGTAA	CGGGCCATGG	GGTATGTACA	TGTAGGGGCT	GAGGTTGGAG	480
GCCTACTAAT	TTCCTGTAGG	GAAGACTCCC	AGCACTTCTG	GAAGTGTGCT	TCTCTTTATT	540
TTTCTACTTC	TCAATTTGAT	GGTTCGATTA	AAGCCTTCTA	GTATCTCAAT	GAAAA	595

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 4..396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28/

CTG	ATG	TCC	GCA	ATT	CTG	AAG	GTT	GGA	CAC	CAC	TGC	TGG	CTG	CCT	GTG	48
Met	Ser	Ala	Ile	Leu	Lys	Val	Gly	His	His	Cys	Trp	Leu	Pro	Val	15	
1				5					10							
ACA	TCC	GCT	GTC	AAT	CCC	CAA	AGG	ATG	CTG	AGG	CCA	CCA	CCA	ACC	GCT	96
Thr	Ser	Ala	Val	Asn	Pro	Gln	Arg	Met	Leu	Arg	Pro	Pro	Pro	Thr	Ala	
				20					25					30		
GTT	TTC	AAC	TGT	GCC	GCT	TGC	TGC	TGT	CTG	TGG	GGG	CAG	ATG	CTG	ATG	144
Val	Phe	Asn	Cys	Ala	Ala	Cys	Cys	Cys	Leu	Trp	Gly	Gln	Met	Leu	Met	
			35					40					45			
AAT	ACA	TAC	CGT	GTA	GTT	CAG	CTT	CCT	GAG	GAG	GCC	AAG	GGC	TTG	GTG	192
Asn	Thr	Tyr	Arg	Val	Val	Gln	Leu	Pro	Glu	Glu	Ala	Lys	Gly	Leu	Val	
		50					55					60				
CCA	CCA	GAG	ATT	CTA	CAG	AAG	TAC	CAT	GGA	TTC	TAC	TCT	TCC	CTC	TTT	240
Pro	Pro	Glu	Ile	Leu	Gln	Lys	Tyr	His	Gly	Phe	Tyr	Ser	Ser	Leu	Phe	
		65				70					75					
GCC	TTG	GTG	AGG	CAG	CCC	AGG	TGG	CTG	CAG	CAT	CTC	TGC	CGT	TGT	GCG	288
Ala	Leu	Val	Arg	Gln	Pro	Arg	Ser	Leu	Gln	His	Leu	Cys	Arg	Cys	Ala	
	80				85				90						95	
CTC	CGC	AGT	CAC	CTG	GAG	GGC	TGT	CTG	CCC	CAT	GCA	CTA	CCG	CGC	CTT	336
Leu	Arg	Ser	His	Leu	Glu	Gly	Cys	Leu	Pro	His	Ala	Leu	Pro	Arg	Leu	
				100					105					110		
CCC	CTG	CCA	CCG	CGC	ATG	CTC	CGC	TTT	CTG	CAG	CTG	GAC	TTT	GAG	GAT	384
Pro	Leu	Pro	Pro	Arg	Met	Leu	Arg	Phe	Leu	Gln	Leu	Asp	Phe	Glu	Asp	
			115					120					125			
CTG	CTC	TAC	TAGGCTTGCT				GCCCTGTGAA			CAAAGCAGAC			CCCACCCCCA			433
Leu	Leu	Tyr														
		130														
CCCCAAGGGC				ATCTCTCAGC			AATGAATGAT			GCAAGGCGGT			CTGTCTTCAA			493
GACGCCTTGA				TCCACACTTG			AGAGAAGAGG			CCAGATCAGC			ACCYGGCTGG			553

AGAGGGCACC TGTGCAGATC TGTGTGCGCA CTGGAAATCT CTAGGCTGAA GGCYAGAGCA 613
AATGGTGCAR GTGTTAGTCC TTGGGANGAG AGACAGANGG TGAGAAAGCA AGACAGAGGT 673
GAGAGTGCAC ATGTCAAGTG GTAGATTGCC TTAAAAGAAA GCTAAAAAAA GAAAAAGATT 733
CGGGCGAACT TCTTTAGGGG TAATGCTGCA GCGTGTTAAA CTGACTGACC AGCGTCCATA 793
TCTTTGGACC CTTCCCGGGT GAAAAAGCCC CTTCATCCTC CAGCGCTCCC CAAGGGTGCT 853
TAGCAATACC GGGTGCTTTT CTGCCGCAAA GTGAGTTACC AAA 896

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ser Ala Ile Leu Lys Val Gly His His Cys Trp Leu Pro Val Thr
1 5 10 15
Ser Ala Val Asn Pro Gln Arg Met Leu Arg Pro Pro Pro Thr Ala Val
20 25 30
Phe Asn Cys Ala Ala Cys Cys Cys Leu Trp Gly Gln Met Leu Met Asn
35 40 45
Thr Tyr Arg Val Val Gln Leu Pro Glu Glu Ala Lys Gly Leu Val Pro
50 55 60
Pro Glu Ile Leu Gln Lys Tyr His Gly Phe Tyr Ser Ser Leu Phe Ala
65 70 75 80
Leu Val Arg Gln Pro Arg Ser Leu Gln His Leu Cys Arg Cys Ala Leu
85 90 95
Arg Ser His Leu Glu Gly Cys Leu Pro His Ala Leu Pro Arg Leu Pro
100 105 110
Leu Pro Pro Arg Met Leu Arg Phe Leu Gln Leu Asp Phe Glu Asp Leu
115 120 125
Leu Tyr
130

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTGGGGGCGT CATCATGACC TCCTCTAGGG CTCTGCAACA TGACTCCTGT GGTGCAAATC	60
AACAAATTGT TCACTGATGA ATCCACAAGG ATCTCTGGGC CTACAACCAG GTCCTGGTCC	120
ACATGACTGT CGTCTTCGGA GAAGGCACCA CTCGCCCCCG GCAGGTACGG CTGACACCTC	180
CATGGGAGAA GACGTATCCA GGCAGCAGCT GCGCGGCCCT TCAAGAGGGC ACATCCCGTC	240
ATCTAAAGGC ACGGTGTACT GAAGGTAGTC CTGAGACATG AGTCCGATTA CTACAGGCAC	300
GTGTTCTCTC AGGTGGAGGC TCAGGTCCCC GGGTGAGCTG GGGCTGCAGC GGGACTCAGG	360
GCGCGGCTCT GGCTGCAGGT CTCGCAGCTC CCTGGGCTGT AGCTCCCGCA GATCCTTGCG	420
CACACCGTTG ACTGGT	436

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTAATAGTAC CTACATAGTA GAAAATTATA ACTCCACTTT AAAACAATGT TTTCTTTCTA	60
TTCAAATCAA TTTAAAACTT TTTATAAACA TTAATGTTGC AAGAGAATCC AGTCCATTTA	120
TGAAAATTAG TTGACAATCA AGTTCACCCA AGAAAATGTT GACTAAGCTA AAGAAATCAC	180
AGATAAAACA TTTTACCAAA AGGATAGGTA ACACACAAAA AAATGCTATC ACAGGAAGCT	240
ATGATCATCT AATATTTCTT TAATAATAAT TCTAGTTCCA TAGGTTTTCA TGTTATGCCA	300
ATTTGTACCC GAGTTTAATT ACAGAAAAGG CAACAATTC TAAATTGGTG GTATACATTT	360
CTTTACAATT TTTTAATGTA AGGCCATTTA TTAAAATAGA CAACTAGAA GATGAAAACG	420

AAGGCAACAG	AAAAATTCAA	CTTTTCACAA	CCAAAAGAAT	TAGCACAACC	TTAGAAATAA	480
TTTAGAAAAA	AGTGTGTGTA	AAAGATATGT	TGCAGATCTC	CGTTCCATTA	CCCAAGATTA	540
TGTCAATTCA	CGATTCTAAA	TAAATCTTTT	TAAAGTAAGA	GATTAAAAAC	TCATCTTCAG	600
TGTATATGTA	AATTCCGTGG	TTTTATCACA	CAGGTATGTT	TATTCAACAC	TGCTTTGGAA	660
ATGGACCATT	TAAAAGGACA	TGGCAATTTC	CATTCTGTTA	AGTTTCATTC	AACCTTTACT	720
TAGGGGTGTA	TTACCACATG	AAATGTGCTT	TTAATGCATA	AAAATCACAG	TGGATTAGCC	780
AGCAAAAGGG	ACTGGGCGGG	GGGGGCATTG	AGGAGAATTT	GATAATTCAC	ATTGTGATTA	840
TTCTGCACAT	TGATGAAACA	TAATTCACAC	CTCTAAAACC	TCAAGACTTC	CCTTTTTTAA	900
AGAACC AAAA	TAAACCCAAG	ACACCTTGCT	GACACTTCCC	CACCCCTAAA	CAAAC TGATG	960
ACTCTTTTAC	ACATAAAACT	GAAATAGTTA	TGGCAGCAAA	AGATTTTGAT	GGCAATGAAA	1020
GTTTGTA AAC	TGTATTTCAA	TCTCTTG TTC	TTATTCCCAA	AGTGCAAGAT	GCAGGGTTCT	1080
CAATCTTTCA	GTAGTGCTTC	TCCTGTAAAT	AATCCTTCAT	TTTGTTTGGC	AAAGGCAGTT	1140
TCTGAATTAA	GTCTATTCTG	GTATACTGAC	GTATAACAAA	ACGACACAGG	TACTGCAACG	1200
AGCGCACCTA	TGAACCCCGG	AACACTGGTT	GGCAAGTTCT	GACGGAAGTG	CAGATTCCAG	1260
GCAGCGAGAC	CTTGAATAAC	AAAAAGCTCC	CATTTTCAGA	GTCCCTGATT	GAATGCTCCA	1320
ATTAGATCAA	CTATGGACGT	ATGTCCTTCC	ACATCGGCTG	TTCATAAAAG	CTAAACCTAC	1380
CATTTGAGTG	CTCAATTCTA	GTGTGAAGTG	TTTTACCATG	GGAGCGAAAG	TCACAGCTTA	1440
AAAGGTAACG	GTCGTCAGAA	CTGTCCCGAA	CAAGAAAAGA	ACCATCTGGC	ACGTTTGCTA	1500
GCTTCCCTTC	TGCCTCCCAA	CGTGTGATTG	GTCCCCAGTA	CCATCCTTGC	TTTGCAAGTT	1560
TTTTCAGCTC	CTCTGTAAGG	CTTGTACAAA	GCATGGGACC	ACTACTTTGC	ACTGAGTCAT	1620
AAACTCTTGC	AACCCAGGA	GCAGAGTTGC	GATCAAAATT	CAAATGACAG	CGCATAACTT	1680
TCAGCCACGT	GGGGCTTTCT	GTCCAGTGAG	TCCACTGAAA	GTTCCCTTTT	GGGATTTGGA	1740
TTATTCCCTGC	ATTGGAGTAA	CCAATGGTGA	AGATTGGAGG	GACATCCATC	GTGAACCCGC	1800
TCTCCGGGGT	TCTGCAACAT	GACTCCCGTG	GTGCCAATCA	ACAAGCCATT	CACCGGACTG	1860
ATCCACGAAG	ATCTCTGGGG	CGACAAC TAG	GTCTGGTCT	ACCTGACTCT	CATCCTCGGG	1920
GAAAGCGCGC	CCTCCC ACTT	GAGGAGGAAC	CGCAGAGACT	TCCATGGGAG	AAGAGCTGTC	1980
CAGACAATAG	CTCCGTGATC	CTTCCAAAGG	ATACATCCCC	TCATCTAAAG	GCACAGTATA	2040
CTGAATGTAG	TCCTGAGGCA	TAAGTCCAAT	AACGACAGGC	ACATGTTTCAT	CCAGGTGAAG	2100

ATGCAGGTCT CCATTATGAG AAGCCGAGCT CTTCAAGTGAA TTGGCTTGCT CCTGGCACGT 2160
GGTCTCAGAC TGGAGGTCGT 2180

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGCACGAGGC TGTGTCCAGC ACACAGAGAG GGCCCGGCCA TCTGCTTTGG TTCAGAGCCC 60
TGTGTCTGTC TGTCACCTAG ACTCTTCCTC CCGGCTCGCA GCTCACCTC CATCCTCCTT 120
ACTGGCTCCA GCATGACTCG CTTCTCTTAT GCAGAGTACT TTGCTCTGTT TCACTCTGGC 180
TCTGCACCTT CCAGGTCCCC TTCGTCTCCC GAGAACCCAC CGGCCCGCGC ACCCCTGGGT 240
CTGTTCCAAG GGGTCATGCA GAAGTATAGC AGCAACCTGT TCAAGACCTC CCAGATGGCG 300
GCTATGGACC CCGTGCTGAA GGCCATCAAG GAAGGGGATG AAGAGGCCTT GAAGATCATG 360
ATCCAGGATG GGAAGAATCT TGCAGAGCCC AACAAGGAGG GCTGGCTGCC GCTCCACGAG 420
GCTGCCTACT ATGGCCAGCT GGGCTGCCTG AAAGTCCTGC AGCAAGCCTA CCCAGGGACC 480
ATTGACCAAC GCACACTGCA GGAAGAGACA GCATTATACC TGGCCACATG CAGAGAACAC 540
CTGGATTGCC TCCTGTCGCT GCTCCAGGCG GGGGCAGAGC CTGACATCTC TAACAAATCC 600
AGGGAGACTC CACTTTACAA AGCCTGTGAG CGCAAGAACG CGGAGGCGGT GAGGATATTG 660
GTGCGATACA ACGCAGACGC CAACCACCGC TGTAACAGGG GCTGGACCGC ACTGCACGAG 720
TCTGTCTCCC GCAATGACCT GGAGGTCATG GAGATCCTAG TGAGTGGCGG GGCCAAGGTG 780
GAGGCCAAGA ATGTCTACAG CATCACCCCT TTGTTTGTGG CTGCCCAGAG TGGGCAGCTG 840
GAGGCCCTGA GGTTCCCTGGC CAAGCATGGT GCAGACATCA ACACGCAGGC CAGTGACAGT 900
GCATCAGCCC TCTACGAGGC CAGCAAGAAT GAGCATGAAG ACGTGGTAGA GTTTCTTCTC 960
TCTCAGGGCG CCGATGCTAA CAAAGCCAAC AAGGACGGCC TGCTCCCCCT GCATGTTGCC 1020
TCCAAGAAGG GCAACTATAG AATAGTGCAG ATGCTGCTGC CTGTGACCAG CCGCACGCGC 1080

GTGCGCCGTA	GCGGCATCAG	CCCGCTGCAC	CTAGCGGCCG	AGCGCAACCA	CGACGCGGTG	1140
CTGGAGGCGC	TGCTGGCCGC	GCGCTTCGAC	GTGAACGCAC	CTCTGGCTCC	CGAGCGCGCC	1200
CGCCTCTACG	AGGACCGCCG	CAGTTCTGCG	CTCTACTTCG	CTGTGGTCAA	CAACAATGTG	1260
TACGCCACCG	AGCTGTTGCT	GCTGGCGGGC	GCGGACCCCA	ACCGCGATGT	CATCAGCCCT	1320
CTGCTCGTGG	CCATCCGCCA	CGGCTGCCTG	CGCACCATGC	AGCTGCTGTT	GGACCATGGC	1380
GCCAACATCG	ACGCCTACAT	CGCCACTCAC	CCCACCGCCT	TTCCAGCCAC	CATCATGTTT	1440
GCCATGAAGT	GCCTGTCGTT	ACTCAAGTTC	CTTATGGACC	TCGGCTGCGA	TGGCGAGCCC	1500
TGCTTCTCCT	GCCTGTACGG	CAACGGGCCG	CACCACCCGC	CCCGCGACCT	GGCCGCTTCC	1560
ACGACGCACC	CGTGGACGAC	AAGGCACCTA	GCGTGGTGCA	GTTCTGTGAG	TTCCTGTCGG	1620
CCCCGGAAGT	GAGCCGCTGG	GCGGGACCCA	TCATCGATGT	CCTCCTGGAC	TATGTGGGCA	1680
ACGTGCAGCT	GTGCTCCCGG	CTGAAGGAGC	ACATCGACAG	CTTTGAGGAC	TGGGCTGTCA	1740
TCAAGGAGAA	GGCAGAACCT	CCGAGACCTC	TGGCTCACCT	CTGCCGGCTG	CGGGTTCGGA	1800
AGGCCATAGG	AAAATACCGG	ATAAACTCC	TGGACACACT	GCCGCTTCCC	GGCAGGCTAA	1860
TCAGATACTT	GAAATATGAG	AATACACAGT	AACCAGCCTG	GAGAGGAGAT	GTGGCCTTCA	1920
GACTGTTTCC	GGGACGCCCC	AGGTGGCCTG	CATCCAGGAC	CCCCTGGGGT	CAGAACAGGT	1980
GTGACCTTGC	TGGTTCTTTG	CTGGAGCTTC	ACCCAAAGTG	AGAACCTGAT	GTGGGGAGTG	2040
GACGTGGAAC	CTCTGCTTTC	ACACTGTCAG	CGGATCGCAG	ACCCGCTCTG	CTTCTGGCCA	2100
TAGCCAGAGA	CCTTCAACCT	GGGGCCAGGG	GAGAGCTGGT	CTGGGCAAGG	TGGCCCAGGC	2160
AGGAATCCTG	GCCTTAAGCT	GGAGAACTTG	TAGGAATCCC	TCACTGGACC	CTCAGCTTTC	2220
AGGCTGCGAG	GGAGACGCCC	AGCCCAAGTA	TTTTATTTCC	GTGACACAAT	AACGTTGTAT	2280
CAGAAAAAAA	AAAAAACATG	GGCGCAGCTT	ATTCCTTAGT	AGGGTATTTA	CTTGCATGCG	2340
CGCTTAAAGC	TACTGGAAAC	ATGCGTTCCA	CTATGCTTGA	GAATCCCCTT	GCACTGGTAA	2400
ACGAGAGCCG	ACGTGCTTCA	AGGTTGCGATT	TTTGGTTGCC	CCTTTGGCGT	TCCGCGGGTT	2460
TGTCCGACGT	AATTGACCCC	GTGTTTTGTC	ACTTTCGAGT	GTTCCGACTA	TTGGGGGGCT	2520
TTTGGTTGTC	CCCAAATTG	TGGGTGGTGT	GCGGACGCCA	CGAGAAGTGG	TTCATGGGCG	2580
ATAATCATTA	CTGGAGAATG	TAGAGCGGCG	GTTTTACGAA	TAAATATTTT	TTAAGCCGCC	2640
TTCCCAAAA						2649

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCTCCTGAGA GTTCGCCGGC CCGGGCCCAA TGGGTTGTTC CAAGGGGTCA TGCAGAAATA	60
CAGCAGCAGC TTGTTCAAGA CCTCCCAGCT GGCGCCTGCG GACCCCTTGA TAAAGGCCAT	120
CAAGGATGCG ATGAAGAGGC CTTGAAGACC ATGATCAAGG AAGGGAAGAA TCTCGCAGAG	180
CCCAACAAGG AGGGCTGGCT GCCGCTGCAC GAGGCCGCAT ACTATGGCCA GGTGGGCTGC	240
CTGAAAGTCC TGCAGCGAGC GTACCCAGGG ACCATCGACC AGCGCACCTT GCAGGAGGAA	300
ACAGCCGTTT ACTTGGAAC GTGCAGGGGC CACCTGGACT GTCTCCTGTC ACTGCTCCAA	360
GCAGGGGCAG AGCGGGACAT CTCCAACAAA TCCCGAGAGA ACCGCTCTAC AAAGCCTGTG	420
AGCGCAAGAA CGCGGAAGCC GTGAAGATTC TTGGTGCAGC ACAACGCAGA CACCAACAAC	480
GCTGCAACCG GGCTG	495

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTGCAGCTCT GCTCGCGGCT GAAGGAACAC ATCGACAGCT TTGAGGACTG GGCCGTCATC	60
AAGGAGAAGG CAGAACCTCC AAGACCTCTG GCTCACCTTT GCCGACTGCG GGTTCGAAAG	120
GCCATTGGGA AATACCGTAT AAAACTCCTA GACACCTTGC CGCTCCCAGG CAGGCTGATT	180
AGATACCTGA AATACGAGAA CACCCAGTAA CTGGGGCCAC GGGGAGAGAG GAGTAGCCCC	240
TCAGACTCTT CTTACTAAGT CTCAGGACGT CGGTGTTCCC AACTCCAAGG GGACCTGGTG	300

ACAGACGAGG CTGCAGGCTG CCTCCCTCTC AGCCTGGACA GCTACCAGGA TCTCACTGGG	360
TCTCAGGGCC CAGAGCTTTG GCCAGAGCAG AGAACAGAAT GTGTCAAGGA GAAGAATCAT	420
TTGTTTACAA ACTGATGAGC AGATCCCAGA CCTTCTCTAC CTTCAGGAAT GGCAGAAACC	480
TCTATTCCTG GGGCCAGGGC AGAGCTTGAG GTGTTCTGGG GAAGGTGGTG CTCAGAGCCT	540
TCCCTGTGCC CCTCCACTTG TTCTGGAAAA CTCACCACTT GACTTCAGAG CTTTCTCTCC	600
AAAGACTAAG ATGAAGACGT GGCCCAAGGT AGGGGGTAGG GCGAGCCTGG GTCTTGGAGG	660
GCTTTGTAA GTATTAATAT AATAAATGTT ACACATGTGA AAAAAAAAAA	709

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTG GAG AAG TGT GGT TGG TAT TGG GGG CCA ATG AAT TGG GAA GAT GCA	48
Leu Glu Lys Cys Gly Trp Tyr Trp Gly Pro Met Asn Trp Glu Asp Ala	
1 5 10 15	
GAG ATG AAG CTG AAA GGG AAA CCA GAT GGT TCT TTC CTG GTA CGA GAC	96
Glu Met Lys Leu Lys Gly Lys Pro Asp Gly Ser Phe Leu Val Arg Asp	
20 25 30	
AGT TCT GAT CCT CGT TAC ATC CTG AGC CTC AGT TTC CGA TCA CAG GGT	144
Ser Ser Asp Pro Arg Tyr Ile Leu Ser Leu Ser Phe Arg Ser Gln Gly	
35 40 45	
ATC ACC CAC CAC ACT AGA ATG GAG CAC TAC AGA GGA ACC TTC AGC CTG	192
Ile Thr His His Thr Arg Met Glu His Tyr Arg Gly Thr Phe Ser Leu	
50 55 60	
TGG TGT CAT CCC AAG TTT GAG GAC CGC TGT CAA TCT GTT GTA GAG TTT	240
Trp Cys His Pro Lys Phe Glu Asp Arg Cys Gln Ser Val Val Glu Phe	
65 70 75 80	

ATT AAG AGA GCC ATT ATG CAC TCC AAG AAT GGA AAG TTT CTC TAT TTC	288
Ile Lys Arg Ala Ile Met His Ser Lys Asn Gly Lys Phe Leu Tyr Phe	
85 90 95	
TTA AGA TCC AGG GTT CCA GGA CTG CCA CCA ACT CCT GTC CAG CTG CTC	336
Leu Arg Ser Arg Val Pro Gly Leu Pro Pro Thr Pro Val Gln Leu Leu	
100 105 110	
TAT CCA GTG TCC CGA TTC AGC AAT GTC AAA TCC CTC CAG CAC CTT TGC	384
Tyr Pro Val Ser Arg Phe Ser Asn Val Lys Ser Leu Gln His Leu Cys	
115 120 125	
AGA TTC CGG ATA CGA CAG CTC GTC AGG ATA GAT CAC ATC CCA GAT CTC	432
Arg Phe Arg Ile Arg Gln Leu Val Arg Ile Asp His Ile Pro Asp Leu	
130 135 140	
CCA CTG CCT AAA CCT CTG ATC TCT TAT ATC CGA AAG TTC TAC TAC TAT	480
Pro Leu Pro Lys Pro Leu Ile Ser Tyr Ile Arg Lys Phe Tyr Tyr Tyr	
145 150 155 160	
GAT CCT CAG GAA GAG GTA TAC CTG TCT CTA AAG GAA GCG CAG CGT CAG	528
Asp Pro Gln Glu Glu Val Tyr Leu Ser Leu Lys Glu Ala Gln Arg Gln	
165 170 175	
TTT CCA AAC AGA AGC AAG AGG TGG AAC CCT CCA CGT AGC GAG GGG CTC	576
Phe Pro Asn Arg Ser Lys Arg Trp Asn Pro Pro Arg Ser Glu Gly Leu	
180 185 190	
CCT GCT GGT CAC CAC CAA GGG CAT TTG GTT GCC AAG CTC CAG CTT TGAAGAACCA	
631	
Pro Ala Gly His His Gln Gly His Leu Val Ala Lys Leu Gln Leu	
195 200 205	
AATTAAGCTA CCATGAAAAG AAGAGGAAAA GTGAGGGAAC AGGAAGGTTG GGATTCTCTG	691
TGCAGAGACT TTGGTTCCCC ACGCAAGCCC TGGGGCTTGG AAGAAGCACA TGACCGTACT	751
CTGCGTGGGG CTCCACCTCA CACCCACCCC TGGGCATCTT AGGACTGGAG GGGCTCCTTG	811
GAAAACTGGA AGAAGTCTCA ACACTGTTTC TTTTTC	848

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 207 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Leu	Glu	Lys	Cys	Gly	Trp	Tyr	Trp	Gly	Pro	Met	Asn	Trp	Glu	Asp	Ala
1				5					10					15	

Glu	Met	Lys	Leu	Lys	Gly	Lys	Pro	Asp	Gly	Ser	Phe	Leu	Val	Arg	Asp
			20					25					30		
Ser	Ser	Asp	Pro	Arg	Tyr	Ile	Leu	Ser	Leu	Ser	Phe	Arg	Ser	Gln	Gly
		35					40					45			
Ile	Thr	His	His	Thr	Arg	Met	Glu	His	Tyr	Arg	Gly	Thr	Phe	Ser	Leu
	50					55					60				
Trp	Cys	His	Pro	Lys	Phe	Glu	Asp	Arg	Cys	Gln	Ser	Val	Val	Glu	Phe
65					70					75					80
Ile	Lys	Arg	Ala	Ile	Met	His	Ser	Lys	Asn	Gly	Lys	Phe	Leu	Tyr	Phe
				85					90					95	
Leu	Arg	Ser	Arg	Val	Pro	Gly	Leu	Pro	Pro	Thr	Pro	Val	Gln	Leu	Leu
			100					105					110		
Tyr	Pro	Val	Ser	Arg	Phe	Ser	Asn	Val	Lys	Ser	Leu	Gln	His	Leu	Cys
	115						120					125			
Arg	Phe	Arg	Ile	Arg	Gln	Leu	Val	Arg	Ile	Asp	His	Ile	Pro	Asp	Leu
	130					135				140					
Pro	Leu	Pro	Lys	Pro	Leu	Ile	Ser	Tyr	Ile	Arg	Lys	Phe	Tyr	Tyr	Tyr
145					150					155					160
Asp	Pro	Gln	Glu	Glu	Val	Tyr	Leu	Ser	Leu	Lys	Glu	Ala	Gln	Arg	Gln
			165						170					175	
Phe	Pro	Asn	Arg	Ser	Lys	Arg	Trp	Asn	Pro	Pro	Arg	Ser	Glu	Gly	Leu
			180					185					190		
Pro	Ala	Gly	His	His	Gln	Gly	His	Leu	Val	Ala	Lys	Leu	Gln	Leu	
	195						200					205			

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTCCAAGCC TAACCCATCT TTGTCGTTTG GAAATTCGGG CCAGTCTAAA AGCAGAGCAC	60
CTTCACTCTG ACATTTTCAT CCATCAGTTG CCACTTCCCA GAAGTCTGCA GAACTATTTG	120
CTCTATGAAG AGGTTTAAAG AATGAATGAG ATTCTAGAAC CAGCAGCTAA TCAGGATGGA	180

GAAACCAGCA AGGCCACCTG ACACAGGTCC TTTAATTCTG TTTAGTCACA AAAGACGGCT	240
TGTGTGACTG TTTGGATTTG GTGATCAAAT GTCCATGTTT ACAGTTGCTT TTCCCAGTTT	300
GTGTCTTTCC CAATATTGTG AACCTTATCC ATCTTGCCTT ACTCAGTTTT ATTTCTAGTG	360
CACTTTGTTG TGTATTATTT GTTTACCTGA CCATTTTCTA CTTTATTCTG CTAATAAACT	420
GTAATTCTGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA	464

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGGGATCGAA AGCGGGGGCT TCTGGGACGC AGCTCTGGAG ACGCGGCCTC GGACCAGCCA	60
TTTCGGTGTA GAAGTGGCAG CACGGCAGAC TGGTCAAACA AATGGATTTT ACAGAGGCTT	120
ACGCGGACAC GTGCTCTACA GTTGGACTTG CTGCCAGGGA AGGCAATGTT AAAGTCTTAA	180
GGAAACTGCT CAAAAGGGC CGAAGTGTCTG ATGTTGCTGA TAACAGGGGA TGGATGCCAA	240
TTCATGAAGC AGCTTATCAC AACTCTGTAG AATGTTTGCA AATGTTAATT AATGCAGATT	300
CATCTGAAAA CTACATTAAG ATGAAGACCT TTGAAGGTTT CTGTGCTTTG CATCTCGCTG	360
CAAGTCAAGG ACATTGGAAA ATCGTACAGA TTCTTTTAGA AGCTGGGGCA GATCCTAATG	420
CAACTACTTT AGAAGAAACG ACACCATTTG TTTTAGCTGT TGAAAATGGA CAGATAGATG	480
TGTTAAGGCT GTTGCTTCAA CACGGAGCAA ATGTTAATGG ATCCCATTCT ATGTGTGGAT	540
GGAACCTCCTT GCACCAGGCT TCTTTTCAGG AAAATGCTGA GATCATAAAA TTGCTTCTTA	600
GAAAAGGAGC AAACAAGGAA TGCCAGGATG ACTTTGGAAT CACACCTTTA TTTGTGGCTG	660
CTCAGTATGG CCAAGCTAGA AAGCTTTGAA GCATACTTAT TTCATCCGGG TGCAAATGTC	720
AATTGTCAAG CCTTGGACAA AGCTACC	747

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CACAAATGGG	ACCATACAAA	AATCTTGGAC	TTGTTAATAA	CCACTTACTA	ACCGGGACCT	60
GTGACACTGG	GCTAAACAAA	GTAAGTCCCT	GTTTACTCAG	CAGTGTTTGG	GGGACATGAA	120
GGATTGCCTA	GAAATATTAC	TCCGGAATGG	TCTACAGCCC	AGACGCCCAG	GCGTGCCTTG	180
TTTTTGGATT	CAGTTCTCCT	GTGTGCATGG	CTTTCCAAAA	GGAGGTGGAG	CTGTAGTTCT	240
TTGGAATTGT	GAACATTCTT	TTGAAATATG	GAGCCCAGAT	AAATGAACTT	CATTTGGCAT	300
ACTGCCTGAA	GTACGAGAAG	TTTTCGATAT	TTCGCTACTT	TTTGAGGAAA	GGTTGCTCAT	360
TGGGACCATG	GAACCATATA	TATGAATTTG	TAAATCATGC	AATTAAAGCA	CAAGCAAAAT	420
ATAAGGAGTG	GTTGCCACAT	CTTCTGGTTG	CTGGATTTGA	CCCACTGATT	CTACTGTGCA	480
ATTCTTGGAT	TGACTCAGTC	AGCATTGACA	CCCTTATCTT	CACTTTGGAG	TTTACTAATT	540
GGAAGACACT	TGCACCAGCT	GTTGAAAGGA	TGCTCTCTGC	TCGTGCCTCA	AACGCTTGGA	600
TTCTACAGCA	ACATATTGCC	CACTGTTCCA	TCCCTGACCC	ATCTTTGTCG	TTTGGA AATT	660
CGGTCCAGTC	TAAAATCAGA	ACGTCTACGG	TCTGACAGTT	ATATTAGTCA	GCTGCCACTT	720
CCCAGAAGCC	TACATAATTA	TTTGCTCTAT	GAAGACG TTC	TGAGGATGTA	TGAAGTTCCA	780
GAACTGGCAG	CTATTCAAGA	TGGATAAATC	AGTGAAACTA	CTTAACACAG	CTAATTTTTT	840
TCTCTGAAAA	ATCATCGAGA	CAAAAGAGCC	ACAGAGTACA	AGTTTTTATG	ATTTTATAGT	900
CAAAAGATGA	TTATTGATTG	TCAGATAGGT	TAGGTTTTTG	GGGGCCAGTA	G TTCAGTGAG	960
AATGTTTATG	TTTACA ACTA	GCCTTCCCAG	TAAAAA AAAAA	AAAAA AAAAA	AAAAA AAAAA	1018

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGGGGGGCTG GGACCTGGGG CGTAACCGTC TCTACCACGA CGGCAAGAAC CAGCCAAGTA 60
AAACATACCC AGCCTTTCTG GAGCCGGACG AGACATTCAT TGTCCCTGAC TCCTTTTTCG 120
TGGCCCTGGA CATGRATGAT GGGACCTTAA GTTTCATCGT GGATGGACAG TACATGGGAG 180
TGGCTTTCCG GGGACTCAAG GGTAAAAAGC TGTATCCTGT AGTGAGTGCC GTCTGGGGCC 240
ACTGTGAGAT CCGCATGCGC TACTTGAACG GACTTGATCC TGAGCCCCTG CCACTCATGG 300
ACCTGTGCCG GCGTTCGGTG CGCCTAGCGC TGGGAAAAGA GCGCCTGGGT GCCATCCCCG 360
CTCTGCCGCT ACCTGCCTCC CTCAAAGCCT ACCTCCTCTA CCAGTGATCC ACATCCCAGG 420
ACCGCCATAC GACAGCCATC TGGTGCCAAR TCACTGAGCC CGTTGGGGTC CGCCGACCCC 480
TGCGCCTGGG ATGGAAGCCC ACCTCAGCCA TGGGCAGACG TGCCCCCTCA TCCTACCGGC 540
TGCCTCTGCT GGGGGAACCT ATGCCAACGG ACTTCTCCCT TCCCAACACT GGCTGAAGCA 600
GCAGCACCCA GGCCCTTCCC TGAACCAGAT GCAGAGAATA AACTATGAAA ACCTCTCTCA 660
GGCGCCTTCT GCTCTCAGGT GGAGTGGGCT GCCCCCACT CTCTGCAGAG AGAGGCTACA 720
CCCACCTGGG GGGTCCTGGG AGGTAAGACT AGTAGGAGGT GCCAGGGCTG ARTCCAAAAG 780
a CAGGAATGGC CAGGAMCAGG CCATACAGAT GAAGCTCAGG ATGTCACATA CCATGGACAM 840
TGAGACAGAA CCCCAGGTTG GAMTTCCCTT GGGCCAACGA GTGCCAGCTT TAATGTCAGC 900
TGCMGGTGCT CTGTGGCCTG TATTTATTCT TTAAACAGTA GCAAAGGCCA TTTATTTATT 960
CCACTTAGAA AGGAAACCTT GGTGGGTGGY TTCCCTCGAT GTGCTTTCCC CCACCTCCCT 1020
GGAATGTGTG TGCCACACCT GTCCTTGTC CAGGCCAGGA CTGTGGCACA TGAGCTGGTG 1080
TGCACAGATA CACGTATGTC GTCGTGCATG ACCCCTGACT AGTTCCTAAG TAGCCCTGCA 1140
CCAAGCACCA GAGCAGACCC CAAGAGAGGC CCGTGCAAGT CCCCATGTCC CCAGGTCCCT 1200
GCTTCTGTTG CCTTGGGACT CATAACCGG CACACGTGTT TCAGCCTCTT GACTTCCATG 1260
AGCTTCGAAT TTTGCCCCCG ATTCTTCTGA TATTTCCCAT TGGCATCCTC CAAAGCTCTG 1320
GGCCTGGAGG GCATTAGGAC ACATGGAATG AGTGGGGTCT CCAGCCCCTG GGAAAGCCAC 1380
TGGCAAGGCA GGATTAGAAA GACCAAGAGC AGGGTGGGGC GCCATGAAGC CTGTATGCCT 1440
CTCAGGCTCA AGACCCCGCC ACACACCCAC TCAAGCCTCA GAAGTGGTGT GTAGGGCAGC 1500
CCCAGGAGAG GAATGCCTGT CCTAGCAGCA CGTACATGGA GCACCCCA CA TGTGCTCCAG 1560

- 158 -

G CTCTAGAATC AACTCCCTAC ATTGGGAATG TAGCO
T GCAGGAAGCT CACGTTC CAT CCCCTGCACC AAGGA
C AGGAGGATTG CTGTCAGTGG TGTACAGAGG TCATG
T GTCCTTTAAG AAAAAGAAAA GAAATCAACT TCCAT
G CACAGGTACA ATAGATGACT TKATTTGTTG AAAAA
A TATTTGTAAG AAGCATT

SEQ ID NO:41:

CHARACTERISTICS:
Length: 134 amino acids
Molecular weight: 13076.9
P/I: 4.27
Isoelectric point: 4.27
Instability: single
Topology: linear

Source: DNA

Description: SEQ ID NO:41:

Leu Gly Arg Asn Arg Leu Tyr His Asp Gly
5 10
Thr Tyr Pro Ala Phe Leu Glu Pro Asp Glu
25 30
Ser Phe Phe Val Ala Leu Asp Met Xaa Asp
40 45
Val Asp Gly Gln Tyr Met Gly Val Ala Phe
55 60
Lys Leu Tyr Pro Val Val Ser Ala Val Trp
70 75
Met Arg Tyr Leu Asn Gly Leu Asp Pro Glu
85 90
Leu Cys Arg Arg Ser Val Arg Leu Ala Leu
105 110
Ala Ile Pro Ala Leu Pro Leu Pro Ala Ser
120 125
Tyr Gln

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ /ID NO:41:

[illegible]

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAGGGTAAAA AACTGTATCC TGTAGTGAGT GCCGTCTGGG GCCACTGTAG ATCCGAATGC	60
GCTACTTGAA CGGACTCGAT CCCGAGACTG CCGCTCATGG ATTTGTGCCG TCGCTCGGTG	120
CGCCTGGCCC TGGGGAGGGA GCGCCTGGGG GAGAACCACA CCTGCCGCTG CCGGCTTCCC	180
TCAAGGCCTA CCTCCTCTAC CAGTGACGTT CGCCATCATA CCGCCAGCGC GACAGCCACC	240
TGGTGCCAAC TCACTGAGCC GCCTG	265

(2) INFORMATION FOR SEQ ID NO:43:

- 61 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2438 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AAGTGGCGGC GGTCCCTGGA GAGCAGGCGG AGGCAGCGGC AAGTCTGACT CTGGGCTGAC	60
CGTGGAGCCG GGGCGGGGGC TGACAGCCAG GCCTCCGCCT GGCGGGAGCC GCACGAGGAG	120
CGGGAGTGGC CGGGCCTCTC TTCCGCGCTT GAGCGAGCGC CGGGTGATGG CGGTGGTGAT	180
GGCGGCAGGC GCTCGGACAG CTCCGCTTGA GCTGAGCTCG GAGAGATCCG TCCAGAAAGT	240
GCCCAGAAGA AACTTCCTCT TAGAAAAGCT GAAAAACACA RTATTTATAA CACTGGAAAT	300
TGTAAAGAAT TTGTTTAAAA TGGCTGAAAA CAATAGTAAA AATGTAGATG TACGGCCTAA	360
AACAAGTCGG AGTCGAAGTG CTGACAGGAA GGATGGTTAT GTGTGGAGTG GAAAGAAGTT	420
GTCTTGGTCC AAAAAGAGTG AGAGTTGTTC TGAATCTGAA GCCATAGGTA CTGTTGAGAA	480

TGTTGAAATT	CCTCTAAGAA	GCCAAGAAAG	GCAGCTTAGC	TGTTTCGTCCA	TTGAGTTGGA	540
CTTAGATCAT	TCCTGTGGGC	ATAGATTTTT	AGGCCGATCC	CTTAAACAGA	AACTGCAAGA	600
TGCGGTGGGG	CAGTGTTTTT	CAATAAAGAA	TTGTAGTGGC	CGACACTCTC	CAGGGCTTCC	660
ATCTAAAAGA	AAGATTCATA	TCAGTGAAC	CATGTTAGAT	AAGTGCCCTT	TCCCACCTCG	720
CTCAGATTTA	GCCTTTAGGT	GGCATTTTAT	TAAACGACAC	ACTGTTCCCTA	TGAGTCCCAA	780
CTCAGATGAA	TGGGTGAGTG	CAGACCTGTC	TGAGAGGAAA	CTGAGAGATG	CTCAGCTGAA	840
ACGAAGAAAC	ACAGAAGATG	ACATACCCTG	TTTCTCACAT	ACCAATGGCC	AGCCTTGTGT	900
CATAACTGCC	AACAGTGCTT	CGTGTACAGG	TGGTCACATA	ACTGGTTCTA	TGATGAACTT	960
GGTCACAAAC	AACAGCATAG	AAGACAGTGA	CATGGATTCA	GAGGATGAAA	TTATAACGCT	1020
GTGCACAAGC	TCCAGAAAAA	GGAATAAGCC	CAGGTGGGAA	ATGGAAGAGG	AGATCCTGCA	1080
GTTGGAGGCA	CCTCCTAAGT	TCCACACCCA	GATCGACTAC	GTCCACTGCC	TTGTTCCAGA	1140
CCTCCTTCAG	ATCAGTAACA	ATCCGTGCTA	CTGGGGTGTC	ATGGACAAAT	ATGCAGCCGA	1200
AGCTCTGCTG	GAAGGAAAGC	CAGAGGGCAC	CTTTTACTT	CGAGATTCAG	CGCAGGAAGA	1260
TTATTTATTC	TCTGTTAGTT	TTAGACGCTA	CAGTCGTTCT	CTTCATGCTA	GAATTGAGCA	1320
GTGGAATCAT	AACTTTAGCT	TTGATGCCCA	TGATCCTTGT	GTCTTCCATT	CTCCTGATAT	1380
TACTGGGCTC	CTGGAACACT	ATAAGGACCC	CAGTGCCTGT	ATGTTCTTTG	AGCCGCTCTT	1440
GTCCACTCCC	TTAATCCGGA	CGTTCCCCTT	TTCCCTTGCA	CATATTTGCA	GAACGGTTAT	1500
TTGTAATTGT	ACGACTTACG	ATGGCATCGA	TGCCCTTCCC	ATTCCTTCGC	CTATGAAATT	1560
GTATCTGAAG	GAATACCATT	ATAAATCAAA	AGTTAGGTTA	CTCAGGATTG	ATGTGCCAGA	1620
GCAGCAGTGA	TGCGGAGAGG	TTAGAATGTC	GACCTGCATA	CATATTTTCA	TTTAATATTT	1680
TATTTTCTT	ATGCCTCTTT	GAATTTTGT	ACAAAGGCAG	TTGAATCAAA	TAAAACGTG	1740
CCCTAAGTTT	TAATTCCAGA	TCAATTTATT	TTTTTTATGA	TACACTTGTT	ATATATTTTT	1800
AAGCAGGTGT	TTGGTTTTGT	TTTTACATA	TAAATTTACA	TATGGTCCAG	GCATATTTAC	1860
AATTTCAAGG	CATTGCATAT	ACATTGAAT	ATTCTGTATT	TTTTAAATAA	TCTTTTGTTC	1920
TTTCCTATGT	GTGAAATATT	TTGCTAATCT	ATGCTATCAG	TATTCTTGTA	TGACCGAATA	1980
GTTACCTATT	CTCTTTTCAT	CTTGAAGATT	TTCAGTAAAG	AGTGTTGTAA	TCAATCCATT	2040
ATAATGTAAT	TGACTTTTGT	AATTTGCCAA	TAGGAGTGTT	AAACAACAAA	ATGATTTAAA	2100
ATGAAACTTA	ATGTATTTTC	ATTTTAAATA	TTAACTAAAC	CAAGTTTGTT	TGTTAGTTAT	2160

TCTAGCCAAT AAGAAAAGAG AATGTAGCAT CCTAGAGGTG TATTTGTTCT GCAGTTTGGC	2220
AGGACCGTCA GTTAGTCCAA ATAAACATCC CCTCAGCGTG GAGGCGAATG GAACCTGTGC	2280
TCCTTTCTTA CGGGAAGCTT TGCAAAGCAA AATAGCAGGG TTACAAGCTT GGAGTTGTTA	2340
AGGCAACTAG AGTTTTCTCT ATTAATTTAT AGACTGTTGT TGCACCTACT TAGCTCTTTT	2400
TTGGGAACTC TAGTTCCCAG GGGAAAATAC CTCGTGCC	2438

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser	Gly	Gly	Gly	Pro	Trp	Arg	Ala	Gly	Gly	Gly	Ser	Gly	Lys	Ser	Asp
1				5				10					15		
Ser	Gly	Leu	Thr	Val	Glu	Pro	Gly	Arg	Gly	Leu	Thr	Ala	Arg	Pro	Pro
			20					25					30		
Pro	Gly	Gly	Ser	Arg	Thr	Arg	Ser	Gly	Ser	Gly	Arg	Ala	Ser	Leu	Pro
			35				40					45			
Arg	Leu	Ser	Glu	Arg	Arg	Val	Met	Ala	Val	Val	Met	Ala	Ala	Gly	Ala
			50			55					60				
Arg	Thr	Ala	Pro	Leu	Glu	Leu	Ser	Ser	Glu	Arg	Ser	Val	Gln	Lys	Val
65					70				75					80	
Pro	Arg	Arg	Asn	Phe	Leu	Leu	Glu	Lys	Leu	Lys	Asn	Thr	Xaa	Phe	Ile
			85						90					95	
Thr	Leu	Glu	Ile	Val	Lys	Asn	Leu	Phe	Lys	Met	Ala	Glu	Asn	Asn	Ser
			100					105					110		
Lys	Asn	Val	Asp	Val	Arg	Pro	Lys	Thr	Ser	Arg	Ser	Arg	Ser	Ala	Asp
			115				120					125			
Arg	Lys	Asp	Gly	Tyr	Val	Trp	Ser	Gly	Lys	Lys	Leu	Ser	Trp	Ser	Lys
			130			135					140				
Lys	Ser	Glu	Ser	Cys	Ser	Glu	Ser	Glu	Ala	Ile	Gly	Thr	Val	Glu	Asn
145					150					155					160

Val Glu Ile Pro Leu Arg Ser Gln Glu Arg Gln Leu Ser Cys Ser Ser
165 170 175

Ile Glu Leu Asp Leu Asp His Ser Cys Gly His Arg Phe Leu Gly Arg
180 185 190

Ser Leu Lys Gln Lys Leu Gln Asp Ala Val Gly Gln Cys Phe Pro Ile
195 200 205

Lys Asn Cys Ser Gly Arg His Ser Pro Gly Leu Pro Ser Lys Arg Lys
210 215 220

Ile His Ile Ser Glu Leu Met Leu Asp Lys Cys Pro Phe Pro Pro Arg
225 230 235 240

Ser Asp Leu Ala Phe Arg Trp His Phe Ile Lys Arg His Thr Val Pro
245 250 255

Met Ser Pro Asn Ser Asp Glu Trp Val Ser Ala Asp Leu Ser Glu Arg
260 265 270

Lys Leu Arg Asp Ala Gln Leu Lys Arg Arg Asn Thr Glu Asp Asp Ile
275 280 285

Pro Cys Phe Ser His Thr Asn Gly Gln Pro Cys Val Ile Thr Ala Asn
290 295 300

91 Ser Ala Ser Cys Thr Gly Gly His Ile Thr Gly Ser Met Met Asn Leu
305 310 315 320

Val Thr Asn Asn Ser Ile Glu Asp Ser Asp Met Asp Ser Glu Asp Glu
325 330 335

Ile Ile Thr Leu Cys Thr Ser Ser Arg Lys Arg Asn Lys Pro Arg Trp
340 345 350

Glu Met Glu Glu Glu Ile Leu Gln Leu Glu Ala Pro Pro Lys Phe His
355 360 365

Thr Gln Ile Asp Tyr Val His Cys Leu Val Pro Asp Leu Leu Gln Ile
370 375 380

Ser Asn Asn Pro Cys Tyr Trp Gly Val Met Asp Lys Tyr Ala Ala Glu
385 390 395 400

Ala Leu Leu Glu Gly Lys Pro Glu Gly Thr Phe Leu Leu Arg Asp Ser
405 410 415

Ala Gln Glu Asp Tyr Leu Phe Ser Val Ser Phe Arg Arg Tyr Ser Arg
420 425 430

Ser Leu His Ala Arg Ile Glu Gln Trp Asn His Asn Phe Ser Phe Asp
435 440 445

Ala	His	Asp	Pro	Cys	Val	Phe	His	Ser	Pro	Asp	Ile	Thr	Gly	Leu	Leu
450						455					460				
Glu	His	Tyr	Lys	Asp	Pro	Ser	Ala	Cys	Met	Phe	Phe	Glu	Pro	Leu	Leu
465					470					475					480
Ser	Thr	Pro	Leu	Ile	Arg	Thr	Phe	Pro	Phe	Ser	Leu	Gln	His	Ile	Cys
				485					490					495	
Arg	Thr	Val	Ile	Cys	Asn	Cys	Thr	Thr	Tyr	Asp	Gly	Ile	Asp	Ala	Leu
			500					505					510		
Pro	Ile	Pro	Ser	Pro	Met	Lys	Leu	Tyr	Leu	Lys	Glu	Tyr	His	Tyr	Lys
	515						520					525			
Ser	Lys	Val	Arg	Leu	Leu	Arg	Ile	Asp	Val	Pro	Glu	Gln	Gln		
530						535					540				

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCTCTGGGC	AAGCCGCCCC	CCCCCACCC	ATCTACCACA	CACACACACA	CACACACACA	60
CACACATTCA	GACCTTGGGG	CAAAAACAAA	GCAAATAAC	AACAACAAA	AACTGCCTG	120
TGAAAGTCC	TTACTTCAGG	AAGGTTGGCA	GATGAGGAGC	AAGGGAACAT	TTTATCAGGA	180
CTGCCACAAA	GGAGTCTTTT	TTTTTAATGG	TTTTTCAAGA	CAGGGTTTCT	CTGTATAGCC	240
CTGGCTGTCC	TGGAGCTCAC	TTTGTAGACC	AGGCTGGCCT	CGAACTCAGA	AATTCGCCTG	300
CCTCTGCCTC	CTGAGTGCTG	GGATTAAAGG	CGTGCAGCAC	CATGTCCAAC	TGGCATTTTC	360
TCAATTAAGG	TTCGTTTCCTT	TCAGATAACT	CTAGGTTCTG	GGTCAAGCTG	ACACAAGGCT	420
ACACAGCACA	GTTTGTATGC	CACATTCAGT	TCAGAAGACA	CCCAACCTCC	CTGGAACTGG	480
AACTTATGCA	CATTTGTGAG	CTTCCACTTG	GGAGTGGGAA	CCTGAACTGG	GTCCTCTGCA	540
AGAGCAGCCG	TGCTCTTAAC	TGCTGAGCCA	TTTCAGCAGC	CTCACATCAG	AATTAAGTTA	600
GAAATTAGCCG	GGTATGAATC	ATACCCTTAG	AATCCTAGCA	TCTGAAAGCA	GAGCTAAGAG	660

AAACAGGGAT TCAAGACCAG CTCTTGGCTA CAGAGCCCGT CCTGTCCTAG GATGGGCTAC 720
AAGAGACTAT TTCAAAGCCA TCCAAACAAC AATAACTACA ACAACAACAA GGTAAAATT 780
AGGCTGGGCA CAGGGTACAC ACCTTTAATG CCAACACTCA GGAGGCAGAG GCAGGCTGAT 840
CAGTGTGAGT TTGAGTTCAA CGTGGTCTAC ATAGGGAGTT CTAGGCCAGC AGAGGTTACA 900
GTCTCTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCACACA CACACACACA CACACACACA 960
CACACACACA CACACACGGT GGCATTATGG GATTTTTTTTGGATAAGGTT TCTCTGTCTA 1020
GCCCTGGCAT AGATTCACCTC TGTAGACTAG GCTAGCCTTG AACTCAGAGA TCCGCCTGCC 1080
TCTGCCTCCC AAGTGCTGGG ATTATAGGTG TTGCACCACC ACTGCCCAGC CACTTTGGGA 1140
TTTTTGAAGT GTTATCAAGA GGCTTTCGAG GAGGTCAAAC TTCAACAGCA ACCTCTCCAT 1200
GATAATGTAG CTAATGATCA AACGACACTC AAAACTTAAC CCTTAAAGCA CACATCCACC 1260
AGACAGCGTG CCCACTCGTA GTTCCATTAC TCAGGAGGCT GAAGCAGGAG GATGAAGGAC 1320
TAAGGCTTCA GCAACCTAGG GAGCCGCAGG GGACAGTAGT CTCAATCCCT ACATTCTCCT 1380
GAACACAGGA GCAGGAGTTC AGGAAGGGTG TCAAGGCCGC TTAGTGATCT TAGGGCCTCA 1440
GGAATGACTA GCTCAGGCAG AGAGAGCAAA GGTCTCCAGT GGAGAAGTCT ACACACACAC 1500
ACACACACAC ACACACACAC ACACACACAC AGAATCCAAG GCGATGACGT CATCAAAGGG 1560
TTAATTCTAG TCTGGGATGG GGGGGAGGGT GGGGCACGCA GCTGTCAGGT GGCTTTGGAA 1620
AAATAAACTG CTGAAGAGTC TGACGCCAGG GAGTCCTGGG AGGGACAAGA GGTTACCCAC 1680
TCAAAGAGTG TGCTCCACAA AGCATGCGCG CTTCTCCACG TCTGGAGTCG TCACTTATTT 1740
TTTGCCTGGA TTCTTTGTAG CCGGTGGGTT CTCAAGGCGG TAAGTGGTGT GGCCGCCGTG 1800
GTCTGGGAGG TGACGATAGG GTTAATCGTC CACAGAGCCC AGGGGCGGAG CGCGGGCGGG 1860
CGTCCGCAGC CCCGCTGGAG CCGGAAGCAG TGGCTGGTCA GGGGCGCTTC TAGCCTTCCC 1920
TATCTGTACT TCCACAGAGG TCTCTGCGAG CTAGGGGGAC AGTGAGGTGC GGGGTAGGGG 1980
CCCGGCGTTA GAGCCAGCAA GGGGACGGTT CACGGTAAGG TCTGAGGGAG AGAGAGCTCC 2040
TGAGAACTT GGGGGGCGCG ACACAGATAG GGTGAAAGCA GAGTGATAGA CCTGGGATGG 2100
TTAGGGGACC AAGGGAAGAC CAGGCTGGTT GGCATACACC GGTGAACGGA TGGGAGTCCT 2160
AGGGAAAGAT GATGCGCCTA ACAGTCCTTT CTGTCTCCAC ACCACTCCAG GGGACGATCC 2220
GGAGCTCAAC TTTCAAAGC GAGACGCCCC AGCAAGCCTG TTTTGAGAAG TTCTTCAGCG 2280
GCTCTCCTCA TGGGCCAGAC GGCCCTGGCA AGGGGCAGCA GCAGCACCCC TACCTCGCAG 2340

GCTCTGTACT	CGGACTTCTC	TCCTCCCGAG	GGCTTGGAGG	AGCTCCTGTC	TGCTCCCCCT	2400
CCTGACCTGG	TTGCCCAACG	GCACCACGGC	TGGAACCCCA	AGGATTGCTC	CGAGAACATC	2460
GATGTCAAGG	AAGGGGGTCT	GTGCTTTGAG	CGGCGCCCTG	TGGCCCAGAG	CACTGATGGA	2520
GTCCGGGGGA	AACGGGGGCTA	TTCGAGAGGT	CTGCACGCCT	GGGAGATCAG	CTGGCCCCCTG	2580
GAGCAAAGGG	GCACACACGC	CGTGGTGGGC	GTGGCCACCG	CCCTCGCCCC	GCTGCAGGCT	2640
GACCACTATG	CGGCGCTTTT	GGGCAGCAAC	AGCGAGTCCT	GGGGCTGGGA	TATTGGGCGG	2700
GGAAAATTGT	ATCATCAGAG	TAAGGGCCTC	GAGGCCCCCC	AGTATCCAGC	TGGACCTCAG	2760
GGTGAGCAGC	TAGTGGTGCC	AGAGAGACTG	CTGGTGGTTC	TGGACATGGA	GGAGGGGACT	2820
CTTGGCTACT	CTATTGGGGG	CACGTACCTG	GGACCAGCCT	TCCGTGGACT	GAAGGGGAGG	2880
ACCCTCTATC	CCTCTGTAAG	TGCTGTTTGG	GGCCAGTGCC	AGGTCCGCAT	CCGCTACATG	2940
GGCGAAAGAA	GAGGTGAGAT	ACGGACTAGG	TGTGGGGAGA	TCACTACTCT	TGGCAATGGT	3000
TTGGGCTGGA	AACTCATGGT	TGGAGCACAG	GAAGTAGGCT	TCTTGTCACT	TTGGCCTGTC	3060
ACTTAGATGG	CCTTGGATCT	AGCTTCACTC	CCAATCCCTA	TTGGATGTGA	TGCACAAATT	3120
CAGAGCCTTT	GGGTCTCCCT	CAGCTGAGGT	GGCGGTGGAA	ATGGAGGAAG	AAGGAAGGGT	3180
GCCTGAGCAG	GATCTCAAGT	TCAAGGATGC	CTGGAGTTGC	TTACTTACCT	TGTCTTCCTT	3240
CTCTCTCCGC	AGTGGAGGAA	CCACAATCCC	TTCTGCACCT	GAGCCGCCTG	TGTGTGCGCC	3300
ATGCTCTGGG	GGACACCCGG	CTGGGTCAAA	TATCCTACTCT	GCCTTTGCCC	CCTGCCATGA	3360
AGCGCTATCT	GCTCTACAAA	TGACCCAGTA	GTACAGGGTG	TGCTGGCACC	CTACCGTGGG	3420
GACAGGTGGA	GAGGCACCCG	CTGGCCTAGA	CAACTTTAAA	AAGCTGGTGA	AGCTGGGGGG	3480
GGGGGGCTGG	ACCCCTTCAC	CTCCCCTTCT	CACAGGAGCA	AGACATATAG	AAATGATATT	3540
AAACACCATG	GCAGCCTGGG	ACAAAGAGGT	TTTTGAAGTA	AAAAATGAGA	TGTATTGTCA	3600
CAACCTGTTT	CATTATTGTT	TTTTGTTTTG	TTTTTACACTC	CCCCACCCCA	GGCTAGAGCC	3660
CCATCACTGT	CTTAAGGAAT	TATGACAACC	CACAAAGCTC	AGGCCCAGGT	GTTTATTTCC	3720
CTTACATGTA	GGATGGTTCA	CAAACACAAT	ACAGGGGCTT	TGGCACCGTG	GGGGAGGGGA	3780
CTATCCCAGG	CCTCTTAGGG	TCTCATGTAT	ACCGAATTCA	GACCCGAAAG	CTCTGAATTT	3840
CTGCATCAGA	CATCCAGTAG	AACTTGGGAG	TGAAGCTAGA	GCCAAGGCCA	TCTAAGTGAC	3900
AGGCCAAAGT	GACACGAAGC	CCACTTCCTG	TGCTCCAACC	ATGAGTTTCC	AGCCCAAACC	3960
AATGGAAGGT	GATTTCACTT	GTCAGGGCCC	AAAGGGACAG	TCAGTTCTAC	TCCCTCCCCT	4020

CACTAGGAGC CACCTTGGTG ACAGTTGATT CTACCCACTG TAAGTGGTAA AGGGATTGGC 4080
 CTGGTCCCAA CCATAATAGG GCGGTGGAAA CGGCTCAGGA GGGTACAGCG TGGATTAGGC 4140
 CACAAGATGG GGCAGATGAT GTCATCAGAA GCATGTGACC GGTGGGAGCA GTTACTAAAC 4200
 TTCTGGGCAA CCTAGTCCAT GCTATGCAGG CAGGTAGAGG GATGGGCAGT GCTCATTGTT 4260
 TGGCATTGAT GATGTCCACA AATTCAGGCT TGAGAGATGC GCCACCCACA AGGAAGCCGT 4320
 CCACGTCAGG CTGGCTTGCC AGCTCTTTGC AGGTTGCTCC AGTCACAGAA CCTGTACCAG 4380
 GAACAAGAAG ACAGTTTGGT CAGGTCTATG ATCAGAACAC TTAAGCCCCA CCTCTCTGTG 4440
 CAAGGCAGCC TCAGTCTGTC TTAGCCCATT TCCGTCTTAG CTAGAGCCAA AGCCACTCAC 4500
 CTCCATAAAT GATCCGGGTG CTCTGAGCCA CCCCATCATT GACATTGGAT TTCAGCCATC 4560
 CCCGGAGCTT CTCGTGTACT TCCTGTGCCT AGAAGGAGGA GGCAGAGCTA CTAAGTAAGC 4620
 TCCTTCCTAT CTATCATTCA AGGAGTAAAA ACCACTGGTT CTCACATAGA GTTGAGTTTC 4680
 CAGAAAAGCC CCGGGACCAG AGAGTGGCAA GGCTCCAATC CCACCAGGCT TGGGAATGAAC 4740
 ATTTTTGGCA AAGTCACTCT CCTTGGTGAG TTGGGGGGCC CTCTGTCTCT AAAGGGGCTT 4800
 GGATGGGCTC CATAGCTGTG TGAGTCTGTT AAAGCCGGAC AGGCTGAGGA GCTCTGGGTA 4860
 GTTACCTGCT GAGGGGTTGC CGTCTTGCCA GTCCCAATGG CCCACACAGG TTCATAGGCC 4920
 AGGACCACCT TGCTCCAGTC TTTCACATTA TCTGTGGGGC AGAGAGGAGA GTGAGTAGGA 4980
 AGGAGCTGAC CCGCCAAGC 4999

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Gly	Gln	Thr	Ala	Leu	Ala	Arg	Gly	Ser	Ser	Ser	Thr	Pro	Thr	Ser
1				5				10						15	
Gln	Ala	Leu	Tyr	Ser	Asp	Phe	Ser	Pro	Pro	Glu	Gly	Leu	Glu	Glu	Leu
		20					25					30			
Leu	Ser	Ala	Pro	Pro	Pro	Asp	Leu	Val	Ala	Gln	Arg	His	His	Gly	Trp
		35				40					45				

Asn Pro Lys Asp Cys Ser Glu Asn Ile Asp Val Lys Glu Gly Gly Leu
 50 55 60
 Cys Phe Glu Arg Arg Pro Val Ala Gln Ser Thr Asp Gly Val Arg Gly
 65 70 75 80
 Lys Arg Gly Tyr Ser Arg Gly Leu His Ala Trp Glu Ile Ser Trp Pro
 85 90 95
 Leu Glu Gln Arg Gly Thr His Ala Val Val Gly Val Ala Thr Ala Leu
 100 105 110
 Ala Pro Leu Gln Ala Asp His Tyr Ala Ala Leu Leu Gly Ser Asn Ser
 115 120 125
 Glu Ser Trp Gly Trp Asp Ile Gly Arg Gly Lys Leu Tyr His Gln Ser
 130 135 140
 Lys Gly Leu Glu Ala Pro Gln Tyr Pro Ala Gly Pro Gln Gly Glu Gln
 145 150 155 160
 Leu Val Val Pro Glu Arg Leu Leu Val Val Leu Asp Met Glu Glu Gly
 165 170 175
 Thr Leu Gly Tyr Ser Ile Gly Gly Thr Tyr Leu Gly Pro Ala Phe Arg
 180 185 190
 Gly Leu Lys Gly Arg Thr Leu Tyr Pro Ser Val Ser Ala Val Trp Gly
 195 200 205
 Gln Cys Gln Val Arg Ile Arg Tyr Met Gly Glu Arg Arg Val Glu Glu
 210 215 220
 Pro Gln Ser Leu Leu His Leu Ser Arg Leu Cys Val Arg His Ala Leu
 225 230 235 240
 Gly Asp Thr Arg Leu Gly Gln Ile Ser Thr Leu Pro Leu Pro Pro Ala
 245 250 255
 Met Lys Arg Tyr Leu Leu Tyr Lys
 260

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTACTTTCTT	TATATCTCCA	TAATTTTATT	TACTATTACT	ACATGATACA	TTATTTTATA	60
AAAGTCTTTG	TAACCTCCTT	AAGGATTCAC	TGCTTAATCT	CCAGTGCTTA	GCACAAATCA	120
TTAAATGCGA	ACCAGAAACT	CTTCCAAATG	TGTTACATCT	ATAACCTCAT	TGGATTCTCA	180
CTACCAACCC	CATGCAATAG	ATACTAATGT	GATCTCTGTC	TTACAGAGGA	AGAAACAGGC	240
ACAGGGAGGT	TCAGTAATTT	GCCCAAGGTC	ATACACACAC	TGGCCTTCAG	GTATTCATGC	300
CCGGGGAGTC	TGGTCCCACA	GCTGGCATGT	TTGCCATTAT	ATTATATTGC	CTCCTTATAG	360
TGTCGGCACT	CATTAAGCAC	ATTGACAGCT	ATGCTTGGTG	AGTGACTACT	ATGTACCCAG	420
CTCTGTGCTA	CATGCTTTAC	CTGGATTATT	TCAACTGCAC	AACAACCCTG	TGAGGTAACT	480
ACCATCATTG	CTCCTATTTT	ACATAACAGA	AAACTACAGA	AATCTGGGGC	TGGGCGTAGT	540
GGCTCATGCC	TGAAATCCCA	GCACTTTGGG	AGACCCTGTC	TCTAAAAAAA	ATTTTTTTTTT	600
GGCCGGACGT	GGTGGCTCAC	ACCTGTAATC	TCAGCACTTT	GGGAGGCTAA	GGCAGGCAGA	660
TCACAAGGTC	AGGAGTTCTA	GACCAGCCTG	GCCAACATGG	CAAAACCCTG	TGTCTACTAA	720
AAATACAAAA	AATAGCTAGG	CGTGGTGGCA	GGTGCCTGTA	ATCCCAGCTA	CTCAGGAGGC	780
TGAGGCAGGA	GAATCCCCTG	AACCTGGGAG	ATGGAGGTTA	CAGAGAGCCG	AGATCGTGCC	840
GCTGCACTCC	AGCCTGGGCA	ACAAGAGCAA	GACTCTGTCT	CGAAAAAAAT	AAAAATAAAA	900
ATAAAAAATAT	TTTTTTTAAAA	ATTAGCTGGG	TGTGGTAGCA	CATGCCTGTA	GTCCCAGCTA	960
CTTGGGAGGC	TGAGGTAGGA	GGATCACTTG	AGCCCAGGAG	GTCAAGGCTG	CAGTGGGCTG	1020
TGATGGCGCC	ACTGCACTCT	AGCCTTGGTG	ACAGCAAGAC	CCTGTCTCAA	AAAAAAAAAAA	1080
AAGAGAAATC	GGGCAACTTC	CCCAAGATCG	CGCAGTTAAC	TAGTGGCATA	GCTTCACTCA	1140
AACTCGAAGT	CTTAATCAGG	ACACTCTACC	AAATGAGATC	AACGGCTCAG	TAATGGATTG	1200
GCATCCAGTA	TGAAGACTGG	ACCAGCAGGG	AGAACTATGA	TGCGTACAGC	CTAGAGCCTG	1260
AAGCAGATTT	CACAGCCTCA	GAGGTGGCAC	AGGCTGACTC	ACAACCCGGG	GCAGAAAGGG	1320
ACCAGCCCAG	AAACAGTGAC	CCAGAATCAC	AGGGAAGTAG	AAATGGGATT	CGGCACAATG	1380
AAGCCCCTCC	TTGACCCCAT	GCTCCTTACC	CTCAGGGGCG	CAGGAGTTAG	TCGCTCAGGC	1440
GGCTCAAAGG	TCTTGACGGT	GGAGAACACC	ATCCCAGGG	ATTCCCGACG	CGGTGATGCC	1500
ATCAAAGCGT	TAATTCTGAG	ATGGGCCTGC	CCGGGTGCGG	ACTCTGCCGC	AGCAAGAGAA	1560
GGGTAACTG	CCCCGGGCCT	TCGCCGTGGG	GGCGGGGCCT	CGGGGAGGGT	CACAGCCCGG	1620

GACTGAGACC	CGAGGTTAAC	CGCCCGGGGT	GGGCTCCACG	GGGGCGGGGC	ATGCTCTCCG	1680
CGGCTGCTGC	CGGTATAGAG	CGGTAACTGC	CCAGGAGGGG	GCGGGGCCCC	ACAGGGGCGT	1740
GGCCTCGGAG	CTGCACGGCC	GTGGGCGGCG	ATGAGAGGGT	TAAGCCCCAG	AGGGCCCTGG	1800
AGGGGCGGGG	CCGCGGGACG	GGCTCGGCCC	AAGGGAGGAG	CTGGGGGCGG	AAGCGGCCGG	1860
CGGTCTGCGC	CCTGCGCGCC	TCGGCTTCTT	TCCGCCCAGG	TCCTTCAGAG	GCCCGGCGAC	1920
CTCCAGGGCT	GGGAAGTCAA	CCGAGGTTCT	GGGGCAGCGG	CGAGGGCTCC	GGGCGAGTAA	1980
GGGGGATGGT	CCATGCTGAG	GCCCAAATGG	GGCGAACTCG	CGAGAGTCTC	TGGCGACCTG	2040
GATCAGATGG	GGCGAGGGCA	GATGAAGGGC	CCAGGAGCTT	TGGGGCAGCG	AGGAGGGAGG	2100
AGCGGGCCCC	TTGGCAAAC	TGGGTGAAAG	GATGGGGTAC	CTGGGTGACG	AGCCCCCGCC	2160
AGGATTCTGC	TCTTCACGCC	CCTTTTCTCC	CAGCTCCCTT	CCAGGTCAAT	CCAAACTGGA	2220
GCTCAACTTT	CAGAAGAGAA	AGACGCCCCA	GCAAGCCTCT	TTCGGGGAGT	CCTCTAGCTC	2280
CTCACCTCCA	TGGGCCAGAC	AGCTCTGGCA	GGGGGCAGCA	GCAGCACCCC	CACGCCACAG	2340
GCCCTGTACC	CTGACCTCTC	CTGTCCCGAG	GGCTTGGAAG	AGCTGCTGTC	TGCACCCCT	2400
CCTGACCTGG	GGGCCAGCG	GCGCCACGGT	TGGAACCCCA	AAGACTGTTC	AGAGAACATC	2460
GAGGTCAAGG	AAGGAGGGTT	GTACTTTGAG	CGGCGGCCCC	TGGCCCAGAG	CACTGATGGG	2520
GCCCGGGGTA	AGAGGGGCTA	TTCAAGGGGC	CTGCACGCCT	GGGAGATCAG	CTGGCCCCCTA	2580
GAGCAGAGGG	GCACGCATGC	CGTGGTGGGC	GTGGCCACGG	CCCTCGCCCC	GCTGCAGACT	2640
GACCACTACG	CGGCGCTGCT	GGGCAGCAAC	AGCGAGTCGT	GGGGCTGGGA	CATCGGGCGG	2700
GGGAAGCTGT	ACCATCAGAG	CAAGGGGCCC	GGAGCCCCC	AGTATCCAGC	GGGAACTCAG	2760
GGTGAGCAGC	TGGAGGTGCC	AGAGAGACTG	CTGGTGGTTC	TGGACATGGA	GGAGGGAAC	2820
CTGGGCTACG	CTATTGGGGG	CACCTACCTG	GGGCCAGCAT	TCCGCGGACT	GAAGGGCAGG	2880
ACCCTCTATC	CGGCAGTAAG	CGCTGTCTGG	GGCCAGTGCC	AGGTCCGCAT	CCGCTACCTG	2940
GGCGAAAGGA	GAGGTGAGGC	CTGGGGCAGA	CGTGGGGAGA	ACTTTCTGTC	CCTGGTGGCA	3000
GTGGTTTGGG	ATGGAAACTC	TTCTGACAAG	AGCAGAGGGG	ATGGACCTTC	ATCCAGCCTG	3060
CCTCAACCTC	TGTTCAAGTGC	TGGGAAAGGC	TAGGGGTCTT	CACAGCTGTT	ATTTAATTTA	3120
ACCCAACAGC	AATAGAGGTG	AAACAGGCTT	GAGAAAGCAA	CTTTCTCAAG	TTCTCTTGGC	3180
CAGTAAATGG	TGAACCTTCA	GAATGGAGGG	AGGAACTGCA	GGGATGAGAG	AATTCAGGAG	3240
ATATCAACCC	CTGAGCAAGA	GGTGCAAAGC	GTTAGGTACT	GGGTTTGATG	TACAGGTCCA	3300

AAAGAAGGAT	GGGCAGAGCC	AGGTACCCAG	GCTGTATACC	GGATTCCTTG	GGCTCTAACC	3360
TGTCTCTGTG	CCACATACCT	ACTTCCTTCC	TCAGCCACAC	CTCTGGATGG	AGACACTGGG	3420
GCCCTGGGCA	CCAGGGAGGA	GAGCAGTGGA	GGAGGCAGGG	CTTAGGGTG	GGGCAGCAGG	3480
GGAGGAGCCT	CCCCAGGAAC	TGACTGGGTC	CAGGGCTTGG	AGCTGCTCTC	TGCAGTTGTG	3540
TGGGCTGTAG	AGTGGAGGGC	CATCCCTCCT	CACCTCAGCC	CCAGCTCCCA	AGCCTCTGGA	3600
GTCAAAGCCT	GGGCCAGCTC	CACCACTGTC	AGAGCCACCT	TGGCCTGTTG	TTTAGAGGGC	3660
CTTAGCCAGC	TCTTCACCCC	CAGCTCTGAC	TAGGGATGTG	TGAAATCTTA	TCTGGGAGGC	3720
AGAACTTCCG	GGTATCTCAA	ATTCCCCTTT	CAGCCAGGTG	GGCACACTCG	AAGCAGGAAA	3780
GCAGAAAGGC	ATCTGAGTAG	GACCCCGTAG	TTTGAGGACA	TCTGGCTGGT	GGCTGCACCC	3840
ATACTTACAT	TCCCCTCCTT	CTCTCTCCCA	GCGGAGCCAC	ACTCCCTTCT	GCACCTGAGC	3900
CGCCTGTGTG	TGCGCCACAA	CCTGGGGGAT	ACCCGGCTCG	GCCAGGTGTC	TGCCCTGCCC	3960
TTGCCCCCTG	CCATGAAGCG	CTACCTGCTC	TACCAGTGAG	CCCTGTGATA	CCACAGACTG	4020
TGCTGAGGTC	TTGCCACCAC	CCCTCCCCCT	GGGGAGGTGG	GGAGGCACTG	CTGGCCTAGA	4080
CCAGCTGCTG	AAAGCTGGTG	AGGCTGAGCC	CCTACCCCAA	CCCAAGCTCT	GCGGAAATCA	4140
ACAGCCCCAG	AGCCACTTGG	AGGGAGGAAG	AAAGGGAGCC	GGCGTTCAAG	GCTATGACAG	4200
TCTGCTACGC	AAAACATTTT	TTCAAGTAAA	AATAGTAAGA	GATGTTGTTA	TAGAAACCTG	4260
TTCTTGTTTT	TTTTTTTTTC	TTGCACAAAT	GATCATTTAT	ATAGCTGCCT	CAAAAAGGAA	4320
GATTATCTGG	GCAAGTCCAG	TGAAGGCAGA	CAAACCACAA	GACCTAGTGC	CAGGTTTATT	4380
CCCTCACATG	GGTGGTTCAC	ATACACAGCA	CAGAGGCACG	GGCACCATGG	GAGAGGGCAG	4440
CACTCCTGCC	TTCTGAGGGG	ATCTTGCCCT	CACGGTGTA	GAAGGGAGAG	GATGGTTTCT	4500
CTTCTGCCCT	CACTAGGGCC	TAGGGAACCC	AGGAGCAAAT	CCCACCACGC	CTTCCATCTC	4560
TCAGCCAAGG	AGAAGCCACC	TTGGTGACGT	TTAGTTCCAA	CCATTATAGT	AAGTGGAGAA	4620
GGGATTGGCC	TGGTCCCAAC	CATTACAGGG	TGAAGATATA	AACAGTAAAG	GAAGATACAG	4680
TTTGGATGAG	GCCACAGGAA	GGAGCAGATG	ACACCATCAG	AAGCATATGC	AGGGAAAGGG	4740
CAGTTACTGG	GCTTCTGGGC	TGCTTAGTCC	CTGGCTTGGC	AGGAAGGGTA	GGGAAGATGG	4800
ATGGGGCTCA	TTGTTTGGCA	TTGATGATGT	CCACGAATTC	GGGCTTGAGG	GAAGCACCAC	4860
CCACAAGGAA	GCCATCCACA	TCAGGCTGGC	TGGCCAGCTC	CTTGCAGGTT	GCCCCAGTCA	4920
CAGAGCCTGG	GAAGGGAGCA	GAACAAGGGC	TTGGTCAAGA	ATGGGATGAG	TCTGCCCCAT	4980

CCCCACCTCC	ATGTCCGAGG	GCTCAGTCTA	GTCCTCAGCC	CACTCCACCT	CAGCCGGGAA	5040
CCAAAGCCAC	TCACCTCCAT	AAATGATACG	GGTGCTCTGA	GCCACCGCAT	CAGAGACGTT	5100
GGACTTCAGC	CATCCTCGGA	GCTTCTCGTG	TACTTCCTGG	GCCTAGAACA	AGAAGCTGGC	5160
CTAAGTAAGA	CCTTTTCTGC	CTCTCTAAGA	GGAAAAATCA	CTGGCACCAG	TGGACACTTA	5220
GTGTGGTTTC	TGACTGAGTC	AGAGTACCAG	GGCTCTGATC	CAAGCCAGGC	CCTGGACTGG	5280
ATGCCCTTGG	ACAAGTCACT	GTCTCTGGGT	TCAAGGTCTC	TGTGTCTTTG	AAATAAGGGG	5340
TTGCCCCATG	TGGGCTGTGT	CTGTCCAAAC	CTATTGAGGC	AGGCTGGGAT	GAGGGCAGGG	5400
CTCCTGGGCC	CGGTTACCTG	TTGGGGTGTT	GCAGTCTTGC	CAGTACCAAT	GGCCCACACA	5460
GGCTCATAGG	CCAGGACGAC	CTTGCTCCAG	TCCTTCACGT	TATCTGCAGG	GCAGAGATAC	5520
AGATGGAGGG	AAGGGTGAAC	AAGAAAGAGC	TCTCCAGCCA	GGTTCTCCGG	AGTACGAAGA	5580
ACGGTGGCCT	ACTGCCCCCT	AGTGGACATT	GGGGG			5615

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Gly	Gln	Thr	Ala	Leu	Ala	Gly	Gly	Ser	Ser	Ser	Thr	Pro	Thr	Pro
1				5					10					15	
Gln	Ala	Leu	Tyr	Pro	Asp	Leu	Ser	Cys	Pro	Glu	Gly	Leu	Glu	Glu	Leu
		20						25					30		
Leu	Ser	Ala	Pro	Pro	Pro	Asp	Leu	Gly	Ala	Gln	Arg	Arg	His	Gly	Trp
		35					40					45			
Asn	Pro	Lys	Asp	Cys	Ser	Glu	Asn	Ile	Glu	Val	Lys	Glu	Gly	Gly	Leu
		50				55					60				
Tyr	Phe	Glu	Arg	Arg	Pro	Val	Ala	Gln	Ser	Thr	Asp	Gly	Ala	Arg	Gly
65					70					75				80	
Lys	Arg	Gly	Tyr	Ser	Arg	Gly	Leu	His	Ala	Trp	Glu	Ile	Ser	Trp	Pro
				85					90					95	

Leu Glu Gln Arg Gly Thr His Ala Val Val Gly Val Ala Thr Ala Leu
100 105 110

Ala Pro Leu Gln Thr Asp His Tyr Ala Ala Leu Leu Gly Ser Asn Ser
115 120 125

Glu Ser Trp Gly Trp Asp Ile Gly Arg Gly Lys Leu Tyr His Gln Ser
130 135 140

Lys Gly Pro Gly Ala Pro Gln Tyr Pro Ala Gly Thr Gln Gly Glu Gln
145 150 155 160

Leu Glu Val Pro Glu Arg Leu Leu Val Val Leu Asp Met Glu Glu Gly
165 170 175

Thr Leu Gly Tyr Ala Ile Gly Gly Thr Tyr Leu Gly Pro Ala Phe Arg
180 185 190

Gly Leu Lys Gly Arg Thr Leu Tyr Pro Ala Val Ser Ala Val Trp Gly
195 200 205

Gln Cys Gln Val Arg Ile Arg Tyr Leu Gly Glu Arg Arg Ala Glu Pro
210 215 220

His Ser Leu Leu His Leu Ser Arg Leu Cys Val Arg His Asn Leu Gly
225 230 235 240

Asp Thr Arg Leu Gly Gln Val Ser Ala Leu Pro Leu Pro Pro Ala Met
245 250 255

Lys Arg Tyr Leu Leu Tyr Gln
260

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGCTAGATCT GGACCCTACA ATGGCAGC

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 173 -

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGCTAGATCT GCCATCCTAC TCGAGGGGCC AGCTGG

36